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OM nucleic - nucleic search, using sw model

Run on: May 11, 2004, 11:32:23 ; Search time 6027 Seconds
(without alignments)
10945.429 Million cell updates/sec

Title: US-09-807-949B-1

Perfect score: 1522

Sequence: 1 acagtcagcgcgatgctcc.....ttaaaataaatttataat 1522

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_htg.*

3: gb_in.*

4: gb_em.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

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9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_om.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pl.*

26: em_ro.*

27: em_sts.*

28: em_un.*

29: em_vi.*

30: em_htg_hum.*

31: em_htg_inv.*

32: em_htg_other.*

33: em_htg_mus.*

34: em_htg_pln.*

35: em_htg_rod.*

36: em_htg_mam.*

37: em_htg_vrt.*

38: em_sy.*

39: em_htgo_hum.*

40: em_htgo_mus.*

41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|--------------------|
| 1 | 1522 | 100.0 | 1522 | 6 | AR074439 Sequence |
| 2 | 1522 | 100.0 | 1522 | 6 | AR081119 Sequence |
| 3 | 1522 | 100.0 | 1522 | 6 | AR085316 Sequence |
| 4 | 1522 | 100.0 | 1522 | 6 | AR088064 Sequence |
| 5 | 1522 | 100.0 | 1522 | 6 | AR104223 Sequence |
| 6 | 1522 | 100.0 | 1522 | 6 | AR143487 Sequence |
| 7 | 1522 | 100.0 | 1522 | 6 | AR171392 Sequence |
| 8 | 1522 | 100.0 | 1522 | 6 | AR171563 Sequence |
| 9 | 1522 | 100.0 | 1522 | 6 | BD243152 MN gene a |
| 10 | 1522 | 100.0 | 1522 | 6 | AX330007 Sequence |
| 11 | 1522 | 100.0 | 1522 | 6 | AX332607 Sequence |
| 12 | 1522 | 100.0 | 1522 | 6 | AX333244 Sequence |
| 13 | 1522 | 100.0 | 1522 | 6 | AX336174 Sequence |
| 14 | 1522 | 100.0 | 1522 | 9 | HSMATURN |
| 15 | 1520.4 | 99.9 | 1639 | 9 | BC014950 |
| 16 | 1517.4 | 99.7 | 1519 | 9 | HAI10588 |
| 17 | 1399 | 91.9 | 1399 | 6 | AR095263 Sequence |
| 18 | 759.2 | 49.9 | 1965 | 10 | MMU245857 |
| 19 | 457.8 | 30.1 | 1671 | 10 | AB086322 Mus muscu |
| 20 | 414.4 | 27.2 | 6521 | 6 | AX795690 Sequence |
| 21 | 414.4 | 27.2 | 6521 | 6 | AX822141 Sequence |
| 22 | 414.4 | 27.2 | 10898 | 6 | AX825781 Sequence |
| 23 | 414.4 | 27.2 | 10898 | 6 | AR074442 Sequence |
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| 25 | 414.4 | 27.2 | 10898 | 6 | AR085319 Sequence |
| 26 | 414.4 | 27.2 | 10898 | 6 | AR088067 Sequence |
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| 30 | 414.4 | 27.2 | 10898 | 6 | AR171566 Sequence |
| 31 | 414.4 | 27.2 | 10898 | 6 | BD243155 MN gene a |
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| 34 | 413.4 | 27.2 | 415 | 6 | AR074454 Sequence |
| 35 | 413.4 | 27.2 | 415 | 6 | AR081134 Sequence |
| 36 | 413.4 | 27.2 | 415 | 6 | AR085331 Sequence |
| 37 | 413.4 | 27.2 | 415 | 6 | AR088079 Sequence |
| 38 | 413.4 | 27.2 | 415 | 6 | AR104238 Sequence |
| 39 | 413.4 | 27.2 | 415 | 6 | AR143502 Sequence |
| 40 | 413.4 | 27.2 | 445 | 6 | AR171406 Sequence |
| 41 | 413.4 | 27.2 | 445 | 6 | AR171577 Sequence |
| 42 | 413.4 | 27.2 | 445 | 6 | BD243167 MN gene a |
| 43 | 380.2 | 25.0 | 10898 | 9 | HSMNCA9 |
| 44 | 303.8 | 20.0 | 408 | 6 | AX198178 Sequence |
| 45 | 303.8 | 20.0 | 521 | 6 | AX197674 Sequence |

ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION Sequence 1 from patent US 5955075.
ACCESSION AR074439
VERSION AR074439.1 GI:10001194
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1522)
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE Method of inhibiting tumor growth using antibodies to MN protein
JOURNAL Patent: US 5955075-A 1 21-SEP-1999;
FEATURES Location/Qualifiers

AR074439 1522 bp DNA linear PAT 28-AUG-2000

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| | Matches 1522; Conservative | 0; Mismatches 0; Indels 0; Gaps 0 |
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| Qy | 61 | CCTGCTCCAGSCCTCACTGTGCAACTGTCTGTCACTGTGCTTTCTGATGCTTCTCCAT 120 |
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| Db | 121 | CCCAGAGGTTGCCCCGATGCAGAGGATTCCCTTTGGGAGGAGGCTCTTCTCGGGAA 180 |
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| Qy | 301 | GAAGTTAAGCCTTAATCAGAAGAGAGGSCCTCCCTGAAGTTAGAGGATCTACTACTGTT 360 |
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| Qy | 361 | GAGGCTCTCGAGATCTCTCAAGAACCCAGAAATAATGCCCAAGGAGGAGGATCTACT 420 |
| Db | 361 | GAGGCTCTCGAGATCTCTCAAGAACCCAGAAATAATGCCCAAGGAGGAGGATCTACT 420 |
| Qy | 421 | GACCAAGTCAATTGGCGCTATGAGGCGAACCGCGCCTGCGCCCGGGGTGCCACGCTGC 480 |
| Db | 421 | GACCAAGTCAATTGGCGCTATGAGGCGAACCGCGCCTGCGCCCGGGGTGCCACGCTGC 480 |
| Qy | 481 | CGCGGCGCTTCCAGTCCCGGTGGATATCGCGCCCGAGCTCGCGCCTTCTGCGCCGCC 540 |
| Db | 481 | CGCGGCGCTTCCAGTCCCGGTGGATATCGCGCCCGAGCTCGCGCCTTCTGCGCCGCC 540 |
| Qy | 541 | CTCGCCCCCTTGAACTCTCTGGGCTTCCAGTCTCCCGCCGCTCCCAAGACTGCGCTGCGC 600 |
| Db | 541 | CTCGCCCCCTTGAACTCTCTGGGCTTCCAGTCTCCCGCCGCTCCCAAGACTGCGCTGCGC 600 |
| Qy | 601 | AACAATGGCCACAGTGTGCAACTGACCTGCTCTGGGCTAGAGATGGCTCTGGGTCCC 660 |
| Db | 601 | AACAATGGCCACAGTGTGCAACTGACCTGCTCTGGGCTAGAGATGGCTCTGGGTCCC 660 |
| Qy | 661 | GGGCGGAGTAGTCCGGGCTCTGACGTGCTATGTCACCTGGGGGCTCGAGGTGCTCCGGGC 720 |
| Db | 661 | GGGCGGAGTAGTCCGGGCTCTGACGTGCTATGTCACCTGGGGGCTCGAGGTGCTCCGGGC 720 |
| Qy | 721 | TGCGAGCACTGTGGAAGGCCACCGTTTCCCTGCGCGAGATCCAAGTGGTTCACTCAAGC 780 |
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| Qy | 781 | ACCGCTTTGCGACAGTTTGACGAGGCTTTGGGGCGCCCGGAGGCGCTCGCCGTTGTGGCC 840 |
| Db | 781 | ACCGCTTTGCGACAGTTTGACGAGGCTTTGGGGCGCCCGGAGGCGCTCGCCGTTGTGGCC 840 |
| Qy | 841 | GCCTTTCTGGAGGAGGGCCCGGAAGAAAACAGTGGCTATGACAGTTGCTGCTCGCTTG 900 |
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RESULT 3
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LOCUS AR085316 1522 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 1 from patent US 5981711.
ACCESSION AR085316
VERSION AR085316.1 GI:10012085
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 1522)
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE MN-specific antibodies and hybridomas
JOURNAL Patent: US 5981711-A 1 09-NOV-1999;
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Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DEFINITION Sequence 1 from patent US 5989838.
ACCESSION AR088064
VERSION AR088064.1 GI:10014827
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1522)
AUTHORS Zavada, J.; Pastorekova, S. and Pastorek, J.
TITLE Immunological methods of detecting MN proteins and MN polypeptides
JOURNAL Patent: US 5989838-A 1 23-NOV-1999;
FEATURES Location/Qualifiers
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/organism="unknown"
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ORIGIN
Query Match 100.0%; Score 1522; DB 6; Length 1522;
Best Local Similarity 100.0%; Pred. No. 3.4e-311;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DEFINITION Sequence 1 from patent US 6093548.
ACCESSION AR104223
VERSION AR104223.1 GI:12816931
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 1522)
AUTHORS Zavada, J., Pastorekova, S. and Pastorek, J.
TITLE Detection and quantitation of MN-specific antibodies
JOURNAL Patent: US 6093548-A 1 25-JUL-2000;
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VERSION AR143487.1 GI:15104773
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AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1522)
Zavada, J., Pastorekova, S. and Pastorek, J.
MN gene and protein
Patent: JP 2002528085-A 1 03-SEP-2002;
INSTITUTE OF VIROLOGY
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PN JP 2002528085-A/1
PD 03-SEP-2002
PF 22-OCT-1999 JP 2000578465
PR 23-OCT-1998 US 09/177776, 23-OCT-1998 US 09/178115 PI
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ACCESSION
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VERSION

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REFERENCE 1
AUTHORS Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,
Horzigan, S., Soppet, D.R. and Weaver, Z.
TITLE Cancer gene determination and therapeutic screening using signature
gene sets
JOURNAL Patent: WO 0194629-A 516 13-DEC-2001;
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Best Local Similarity 100.0%; Pred. No. 3.4e-311; Indels 0; Gaps 0;
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VERSION AX332607.1 GI:18123241
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,
Horzigan, S., Soppet, D.R. and Weaver, Z.
TITLE Cancer gene determination and therapeutic screening using signature
gene sets
JOURNAL Patent: WO 0194629-A 3116 13-DEC-2001;
Avalon Pharmaceuticals (US)

FEATURES source Location/Qualifiers

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ORIGIN

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Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DEFINITION Sequence 6683 from Patent WO0194629.
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VERSION AX336174.1 GI:18126893
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Young, P. E., Augustus, M., Carter, K. C., Ebner, R., Endress, G.,
Horrikan, S., Soppet, D. R. and Weaver, Z.
TITLE Cancer gene determination and therapeutic screening using signature
gene sets
JOURNAL Patent: WO 0194629-A 6683 13-DEC-2001;
Avalon Pharmaceuticals (US)
FEATURES
source location/Qualifiers
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ORIGIN
Query Match 100.0%; Score 1522; DB 6; Length 1552;
Best Local Similarity 100.0%; Pred. No. 3,4e-311;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1552)
 AUTHORS Pastorek J.
 DIRECT SUBMISSION
 TITLE Submitted (11-JUN-1992) J. Pastorek, Institute of Virology, Slovak
 JOURNAL Academy of Sciences, Dubravska 9, 842 46 Bratislava, SLOVAK
 REPUBLIC
 REMARK revised by [3] MAT
 REFERENCE 2 (bases 1 to 1552)
 AUTHORS Pastorek J., Pastorekova S., Callebaut J., Mornon J., Zelnik V.,
 Opavsky R., Zalcovicova M., Liao S., Portetelle D., Stanbridge E.J.,
 Zavada J. and Burny A.
 TITLE Cloning and characterization of MN, a human tumor-associated
 protein with a domain homologous to carbonic anhydrase and a
 putative helix-loop-helix DNA binding segment
 JOURNAL Oncogene 9 (10), 2877-2888 (1994)
 MEDLINE 94366734
 PUBMED 8084592
 REFERENCE 3 (bases 1 to 1552)
 AUTHORS Pastorek J.
 DIRECT SUBMISSION
 TITLE Submitted (19-JUL-1994) J. Pastorek, Institute of Virology, Slovak
 JOURNAL Academy of Sciences, Dubravska 9, 842 46 Bratislava, SLOVAK
 REPUBLIC
 REMARK revised by [4] MAT
 REFERENCE 4 (bases 1 to 1552)
 AUTHORS Pastorek J.
 DIRECT SUBMISSION
 TITLE Submitted (28-SEP-1995) J. Pastorek, Institute of Virology, Slovak
 JOURNAL Academy of Sciences, Dubravska 9, 842 46 Bratislava, SLOVAK
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Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Uedin, T.B., Toehiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Aramzon, R.D., Mullahy, S.J., Bosak, S.A., McSwan, P.J., McKernan, K.J., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Worley, K.C., Kelleman, M., Sodergren, E.J., Lu, X., Gibbs, R.A., Vallalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kelleman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickerson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalhus, D.E., Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16999-16903 (2002)

22388257

12477932

2 (bases 1 to 1639)

Strausberg, R.

Direct Submission

Submitted (01-OCT-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgapsb-x@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada

info@bcsc.bc.ca

Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo San Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Lilaea Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smalhus, Michael Smith, Lorraine Spence, Jeff Scott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAL Plate: 34 Row: i Column: 18

This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 9955947.

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GenCore version 5.1.6
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Post-processing: Minimum Match 0%
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- 3: Geneseqn2000s.*
- 4: Geneseqn2001as.*
- 5: Geneseqn2001bs.*
- 6: Geneseqn2002s.*
- 7: Geneseqn2003as.*
- 8: Geneseqn2003bs.*
- 9: Geneseqn2003cs.*
- 10: Geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | DB ID | Description |
|------------|--------|---------------|--------|-------|-------------|
| 1 | 1522 | 100.0 | 1522 | 2 | AAT09186 |
| 2 | 1522 | 100.0 | 1522 | 3 | AA16540 |
| 3 | 1522 | 100.0 | 1522 | 3 | AA52459 |
| 4 | 1522 | 100.0 | 1552 | 6 | ABL64779 |
| 5 | 1522 | 100.0 | 1552 | 6 | ABL62179 |
| 6 | 1522 | 100.0 | 1552 | 6 | ABL65416 |
| 7 | 1522 | 100.0 | 1552 | 6 | ABL68346 |
| 8 | 1522 | 100.0 | 1552 | 7 | ACC72730 |
| 9 | 1522 | 100.0 | 1552 | 7 | ABZ77284 |
| 10 | 1522 | 100.0 | 1552 | 7 | ABX76385 |
| 11 | 1522 | 100.0 | 1552 | 7 | ABX76124 |
| 12 | 1379.8 | 90.7 | 1833 | 4 | AAH26551 |
| 13 | 1302.8 | 85.6 | 1397 | 2 | AAQ48456 |
| 14 | 414.4 | 27.2 | 6521 | 9 | ADBS3977 |
| 15 | 414.4 | 27.2 | 10897 | 2 | AAT09187 |
| 16 | 414.4 | 27.2 | 10898 | 3 | AA16543 |
| 17 | 414.4 | 27.2 | 10898 | 3 | AA52462 |
| 18 | 413.4 | 27.2 | 445 | 3 | AA16555 |
| 19 | 413.4 | 27.2 | 445 | 3 | AA52474 |
| 20 | 303.8 | 20.0 | 408 | 5 | AAH83009 |
| 21 | 303.8 | 20.0 | 521 | 5 | AAH82505 |
| 22 | 301.6 | 19.8 | 418 | 5 | AAH82742 |
| 23 | 300.8 | 19.8 | 304 | 4 | AA524167 |

| | | | | | | | |
|---|----|-------|------|------|---|----------|-----------|
| C | 24 | 297 | 19.5 | 297 | 4 | AA524411 | Human ova |
| | 25 | 293.8 | 19.3 | 434 | 5 | AAH82384 | Human ova |
| | 26 | 293 | 19.3 | 305 | 4 | AA523827 | Human ova |
| | 27 | 233.4 | 15.3 | 470 | 3 | AA16577 | MN RNA pr |
| | 28 | 233.4 | 15.3 | 470 | 3 | AA52496 | Probe use |
| | 29 | 230.4 | 15.1 | 6521 | 9 | ADBS4141 | Pretrate |
| C | 30 | 230 | 15.1 | 6521 | 9 | ADBS4142 | Pretrate |
| | 31 | 222.4 | 14.6 | 6521 | 9 | ADBS4269 | Pretrate |
| | 32 | 222 | 14.6 | 6521 | 9 | ADBS4270 | Pretrate |
| C | 33 | 194 | 12.7 | 243 | 6 | ABL86991 | Human ova |
| | 34 | 191 | 12.5 | 191 | 3 | AA16565 | Human MN |
| | 35 | 191 | 12.5 | 191 | 3 | AA52484 | Human MN |
| | 36 | 180.4 | 11.9 | 1401 | 3 | AA16576 | Human MN |
| | 37 | 180.4 | 11.9 | 1401 | 3 | AA52495 | 1.4 kb GC |
| | 38 | 171 | 11.2 | 171 | 3 | AA16557 | Human MN |
| | 39 | 171 | 11.2 | 171 | 3 | AA52476 | Human MN |
| | 40 | 158 | 10.4 | 158 | 3 | AA16561 | Human MN |
| | 41 | 158 | 10.4 | 158 | 3 | AA52480 | Human MN |
| | 42 | 145 | 9.5 | 145 | 3 | AA16562 | Human MN |
| | 43 | 145 | 9.5 | 145 | 3 | AA52481 | Human MN |
| | 44 | 143 | 9.4 | 143 | 3 | AA16558 | Human MN |
| | 45 | 143 | 9.4 | 143 | 3 | AA52477 | Human MN |

ALIGNMENTS

RESULT 1
AAT09186
ID AAT09186 standard; cDNA; 1522 BP.
XX
AC AAT09186;
XX
DT 25-MAR-2003 (revised)
DT 19-AUG-1996 (first entry)
XX
DE MuTu putative oncogene MN cDNA.
XX
KW MuTu; endogenous; cellular component; MN; HeLa cell; diagnosis;
KW lymphocytic choriomeningitis virus; LCMV; putative oncogene; treatment;
KW neoplastic; pre-neoplastic; disease; antisense therapy; antibody;
KW vaccine; vertebrate; immunisation; ss.
XX
OS Homo sapiens.

Key Location/Qualifiers
CDS 13..1392
FT /tag= a
XX
XX WO9534650-A2.
XX
XX 21-DEC-1995.
XX
XX 15-JUN-1995; 95WO-US007628.
XX
XX 15-JUN-1994; 94US-00260190.
XX 07-JUN-1995; 95US-00477504.
XX 07-JUN-1995; 95US-00481658.
XX 07-JUN-1995; 95US-00485049.
XX 07-JUN-1995; 95US-00485862.
XX 07-JUN-1995; 95US-00485863.
XX 07-JUN-1995; 95US-00486756.
XX 07-JUN-1995; 95US-00487077.

(CIBA) CIBA CORNING DIAGNOSTICS CORP.
(VIRO-) INST VIROLOGY.
PA
PA Zavada J, Pastorekova S, Pastorek J;
XX
XX WPI; 1996-049679/05.
DR P-PSDB; AAR88058.
XX
XX MN gene, protein and nucleic acid fragments - used as primers and probes

CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
CC cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilms'
CC tumour
XX

SQ Sequence 1552 BP; 302 A; 471 C; 461 G; 318 T; 0 U; 0 Other;

Query Match 100.0%; Score 1522; DB 6; Length 1552;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACAGTCAGCCGATGGCTCCCTGTGCCCCAGCCCCCTGCTCCCTCTGTTGATCCCGGCC 60
Db 31 ACAGTCAGCCGATGGCTCCCTGTGCCCCAGCCCCCTGCTCCCTCTGTTGATCCCGGCC 90
Qy 61 CTGCTCAGGCTCAGTGTGCACTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 120
Db 91 CTGCTCAGGCTCAGTGTGCACTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 150
Qy 121 CCCAGAGGTTGCCCGGATGCAGAGGATTCCTCCCTTGGGAGGAGGCTCTTCTGGGAA 180
Db 151 CCCAGAGGTTGCCCGGATGCAGAGGATTCCTCCCTTGGGAGGAGGCTCTTCTGGGAA 210
Qy 181 GATGACCCACTGGGCGAGGAGATCTGCCAGTGAAGAGGATTCACCCAGAGAGGAGAT 240
Db 211 GATGACCCACTGGGCGAGGAGATCTGCCAGTGAAGAGGATTCACCCAGAGAGGAGAT 270
Qy 241 CCACCCGAGAGGAGATCTACCTGGAGAGGAGATCTACCTGGAGAGGAGATCTACCT 300
Db 271 CCACCCGAGAGGAGATCTACCTGGAGAGGAGATCTACCTGGAGAGGAGATCTACCT 330
Qy 301 GAAGTTAGCTTAATCAGAGAGAGGAGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT 360
Db 331 GAAGTTAGCTTAATCAGAGAGAGGAGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT 390
Qy 361 GAGGCTCTGGAGATCTCAAGAACCCAGAGATATGCCCCAGAGGAAACAAAGAGGGGAT 420
Db 391 GAGGCTCTGGAGATCTCAAGAACCCAGAGATATGCCCCAGAGGAAACAAAGAGGGGAT 450
Qy 421 GACAGAGTCAATGGCGCTATGGAGGAGACCGCGCTGCGCCCGGGGTGTCACGAGCTGC 480
Db 451 GACAGAGTCAATGGCGCTATGGAGGAGACCGCGCTGCGCCCGGGGTGTCACGAGCTGC 510
Qy 481 GCGGCGCTTCCAGTCCCGGTGATATCGCGCCCGAGCTCGCGCTCTGCGCCGCCC 540
Db 511 GCGGCGCTTCCAGTCCCGGTGATATCGCGCCCGAGCTCGCGCTCTGCGCCGCCC 570
Qy 541 CTGCGCCCTCTGGAATCTCTGGGCTTCCAGCTCCCGCGCTCCAGAACTGCGCTGCGC 600
Db 571 CTGCGCCCTCTGGAATCTCTGGGCTTCCAGCTCCCGCGCTCCAGAACTGCGCTGCGC 630
Qy 601 AACATGCGCCACAGTGTGCACTGACCTGCTCTGGGCTAGAGATGGCTCTGGGCTCC 660
Db 631 AACATGCGCCACAGTGTGCACTGACCTGCTCTGGGCTAGAGATGGCTCTGGGCTCC 690
Qy 661 GGGCGGAGTACCGGCTCTGAGCTGATCTGCACTGCGGGGCTGCAAGTGTCTCCGGC 720
Db 691 GGGCGGAGTACCGGCTCTGAGCTGATCTGCACTGCGGGGCTGCAAGTGTCTCCGGC 750
Qy 721 TCGGAGCACACTGTGGAGGCGCACCGTTTCCCTGCGGAGATCCAGTGTGTTCACTCAGC 780
Db 751 TCGGAGCACACTGTGGAGGCGCACCGTTTCCCTGCGGAGATCCAGTGTGTTCACTCAGC 810
Qy 781 ACCGCTTTGCGAGAGTTGACAGAGGCTTGGGCGCCCGGAGGCTGCGCGTGTGGCC 840
Db 811 ACCGCTTTGCGAGAGTTGACAGAGGCTTGGGCGCCCGGAGGCTGCGCGTGTGGCC 870
Qy 841 GCCTTCTGGAGAGGCGCCGAGAAACAGTGTCTATGAGCAGTGTCTGCTGCTGCTG 900
Db 871 GCCTTCTGGAGAGGCGCCGAGAAACAGTGTCTATGAGCAGTGTCTGCTGCTGCTG 930
Qy 901 GAAGAAATCGCTGAGGAGGCTCAGAGACTCAGGTCCCGAGGACTGGACATATCTGCACTC 960

Db 931 GAAGAAATCGCTGAGGAGGCTCAGAGACTCAGGTCCCGAGGACTGACATATCTGCACTC 990
Qy 961 CTGCCCCCTGACTTTACGCGGCTACTTCCNATATGAGGGGTCTCTGACTACACCGCCCTGT 1020
Db 991 CTGCCCCCTGACTTTACGCGGCTACTTCCNATATGAGGGGTCTCTGACTACACCGCCCTGT 1050
Qy 1021 GCCCAGGGTGTCACTGGAGCTGTGTTAAACAGACAGTGTGAGTGTCTAAAGCAGCTC 1080
Db 1051 GCCCAGGGTGTCACTGGAGCTGTGTTAAACAGACAGTGTGAGTGTCTAAAGCAGCTC 1110
Qy 1081 CACACCTCTCTGACACCCCTGTGGGACCTGGTGTGCTCTCGGCTACAGCTGAACCTTCGGA 1140
Db 1111 CACACCTCTCTGACACCCCTGTGGGACCTGGTGTGCTCTCGGCTACAGCTGAACCTTCGGA 1170
Qy 1141 GCGACGAGCCTTTGAATGGCGGAGTGAATTCAGAGCCTCTTCCCTGCTGGAGTGGACAGC 1200
Db 1171 GCGACGAGCCTTTGAATGGCGGAGTGAATTCAGAGCCTCTTCCCTGCTGGAGTGGACAGC 1230
Qy 1201 AGTCTCGGGCTGTGAGCCAGTCCAGCTGAATTCCTGCTGGGTGTGCTGTGACATCCTTA 1260
Db 1231 AGTCTCGGGCTGTGAGCCAGTCCAGCTGAATTCCTGCTGGGTGTGCTGTGACATCCTTA 1290
Qy 1261 GCCCTGTTTTTGGCTCTCTTTTGTGTGTACAGCGTGGCTTCTTGTGTGAGATGAGA 1320
Db 1291 GCCCTGTTTTTGGCTCTCTTTTGTGTGTGTACAGCGTGGCTTCTTGTGTGAGATGAGA 1350
Qy 1321 AGGACGACACAGAGGGGACCAAGGGGGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1380
Db 1351 AGGACGACACAGAGGGGACCAAGGGGGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1410
Qy 1381 ACTGGAGCTAGAGCTGGATCTTGGAGATGTGAGAGCCAGCCAGAGGATCTGAGGG 1440
Db 1411 ACTGGAGCTAGAGCTGGATCTTGGAGATGTGAGAGCCAGCCAGAGGATCTGAGGG 1470
Qy 1441 GGAGCCGGTAACTGCTGCT 1500
Db 1471 GGAGCCGGTAACTGCTGCT 1530
Qy 1501 TTTTAAATTAATATTTTAAAT 1522
Db 1531 TTTTAAATTAATATTTTAAAT 1552

RESULT 5

ABL62179
ID ABL62179 standard; DNA; 1552 BP.
XX ABL62179;
AC AC
XX XX
XX XX
XX 15-MAY-2002 (first entry)
XX
DE Colon adenocarcinoma related gene sequence SEQ ID NO:516.
XX
XX Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW cyclostatic; gene therapy; antineoplastic; Wilms' tumour; adenocarcinoma;
KW gene; ds.
XX
OS Homo sapiens.
XX
XX WO200194629-A2.
XX
XX 13-DEC-2001.
XX
XX 30-MAY-2001; 2001WO-US010838.
XX
XX 05-JUN-2000; 2000US-0209473P.
PR 05-JUN-2000; 2000US-0209531P.
PR 18-SEP-2000; 2000US-0231133P.
PR 18-SEP-2000; 2000US-0233617P.
PR 20-SEP-2000; 2000US-0234009P.
PR 20-SEP-2000; 2000US-0234034P.
PR 20-SEP-2000; 2000US-0234052P.

PR 22-SEP-2000; 2000US-0234509P.
PR 22-SEP-2000; 2000US-0234567P.
PR 22-SEP-2000; 2000US-0234923P.
PR 25-SEP-2000; 2000US-0234924P.
PR 25-SEP-2000; 2000US-0235077P.
PR 25-SEP-2000; 2000US-0235082P.
PR 25-SEP-2000; 2000US-0235134P.
PR 25-SEP-2000; 2000US-0235280P.
PR 26-SEP-2000; 2000US-0235637P.
PR 26-SEP-2000; 2000US-0235638P.
PR 26-SEP-2000; 2000US-0235711P.
PR 27-SEP-2000; 2000US-0235720P.
PR 27-SEP-2000; 2000US-0235840P.
PR 27-SEP-2000; 2000US-0235863P.
PR 28-SEP-2000; 2000US-0236028P.
PR 28-SEP-2000; 2000US-0236032P.
PR 28-SEP-2000; 2000US-0236033P.
PR 28-SEP-2000; 2000US-0236034P.
PR 28-SEP-2000; 2000US-0236109P.
PR 28-SEP-2000; 2000US-0236111P.
PR 29-SEP-2000; 2000US-0236842P.
PR 29-SEP-2000; 2000US-0236891P.
PR 02-OCT-2000; 2000US-0237172P.
PR 02-OCT-2000; 2000US-0237173P.
PR 02-OCT-2000; 2000US-0237278P.
PR 02-OCT-2000; 2000US-0237294P.
PR 02-OCT-2000; 2000US-0237295P.
PR 02-OCT-2000; 2000US-0237316P.
PR 03-OCT-2000; 2000US-0237425P.
PR 03-OCT-2000; 2000US-0237598P.
PR 03-OCT-2000; 2000US-0237604P.
PR 03-OCT-2000; 2000US-0237606P.
PR 03-OCT-2000; 2000US-0237608P.
PR 01-NOV-2000; 2000US-0244867P.
PR 01-NOV-2000; 2000US-0245084P.

(AVAL-) AVALON PHARM.

XX Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI Soppet DR, Weaver J;
XX

DR WPI; 2002-188264/24.

XX Screening for anti-neoplastic agent involves exposing cells to a chemical
PT agent to be tested for anti-neoplastic activity, and determining a change
PT in expression of a gene of a signature gene set.

XX Claim 1; SEQ ID NO 516; 44pp; English.

XX The present invention describes a method (M1) for screening for an anti-
CC neoplastic agent. The method involves exposing cells to a chemical agent
CC to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (I) of a signature gene set, where (I)
CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC to ABL70110), or is at least 95% identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening an
CC anti-neoplastic agent, and can be used for producing a product which is
CC the data collected with respect to the anti-neoplastic agent as a result
CC of M1, and the data is sufficient to convey the chemical structure and/or
CC properties of the agent. M1 can be used in the treatment of cancer such
CC as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
CC cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
CC tumour

XX Sequence 1552 BP; 302 A; 471 C; 461 G; 318 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 1522; DB 6; Length 1552;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAGTCAGCGCATGGCTCCCTGTGCCCCAGCGCCCTGGCTCCCTCTGTGTGATCCCGGCC 60
DB 31 ACAGTCAGCGCATGGCTCCCTGTGCCCCAGCGCCCTGGCTCCCTCTGTGTGATCCCGGCC 90
QY 61 CTGCTCCAGGCTCACTGTGCAACTGCTGCTGTGCACTGCTGCTTCTGATGCTGTCCAT 120
DB 91 CTGCTCCAGGCTCACTGTGCAACTGCTGCTGTGCACTGCTGCTTCTGATGCTGTCCAT 150
QY 121 CCCAGAGGTTGCCCGGATGCAAGGAGGATTCCTGCTGGAGGAGGCTCTCTGGGGAA 180
DB 151 CCCAGAGGTTGCCCGGATGCAAGGAGGATTCCTGCTGGAGGAGGCTCTCTGGGGAA 210
QY 181 GATGACCCACTGGCGGAGGAGGATCTGCCAGTGAAGAGGATTCACCCAGAGAGGAGAT 240
DB 211 GATGACCCACTGGCGGAGGAGGATCTGCCAGTGAAGAGGATTCACCCAGAGAGGAGAT 270
QY 241 CCACCCGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT 300
DB 271 CCACCCGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT 330
QY 301 GAAGTTAAGCTTAATCAGAGAGGAGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT 360
DB 331 GAAGTTAAGCTTAATCAGAGAGGAGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT 390
QY 361 GAGGCTCTGGAGATCTCAAGAACCCAGAGATTAATGCCACAGGAGCAAGAGGGAT 420
DB 391 GAGGCTCTGGAGATCTCAAGAACCCAGAGATTAATGCCACAGGAGCAAGAGGGAT 450
QY 421 GACAGAGTCAATTGGCGCTATGAGGCGAACCGGCCCTGGGCCCGGGGTGTCCTCCAGCTGC 480
DB 451 GACAGAGTCAATTGGCGCTATGAGGCGAACCGGCCCTGGGCCCGGGGTGTCCTCCAGCTGC 510
QY 481 GCGGGCCGCTTCCAGTCCCGGTGGATATCGCCCCCAGCTCGCGGCTCTCTGCCCCGCC 540
DB 511 GCGGGCCGCTTCCAGTCCCGGTGGATATCGCCCCCAGCTCGCGGCTCTCTGCCCCGCC 570
QY 541 CTGCGCCCCCTGGAACTCTCTGGGCTTCCAGTCCCGCGCGCTCCAGAACTCGCGCTGCGC 600
DB 571 CTGCGCCCCCTGGAACTCTCTGGGCTTCCAGTCCCGCGCGCTCCAGAACTCGCGCTGCGC 630
QY 601 AACATGGCCACAGTGTGCAACTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
DB 631 AACATGGCCACAGTGTGCAACTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 690
QY 661 GGGCGGAGTACCGGGCTCTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTG 720
DB 691 GGGCGGAGTACCGGGCTCTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTG 750
QY 721 TCGGAGCACACTGTGGAAGGCCACCGGTTTCCCTGCCGAGATCCACGTTGTTTCACTCAGC 780
DB 751 TCGGAGCACACTGTGGAAGGCCACCGGTTTCCCTGCCGAGATCCACGTTGTTTCACTCAGC 810
QY 781 ACCGCTTTGCGAGTTGACGAGGCTTGGGGGCGCCGGGAGGCTGCGCGTGTGCTGCTGCTG 840
DB 811 ACCGCTTTGCGAGTTGACGAGGCTTGGGGGCGCCGGGAGGCTGCGCGTGTGCTGCTGCTG 870
QY 841 GCCTTTCTGAGGAGGCGCCGGGAGAAACAGTCCCTATGAGCAGTGTGCTGCTGCTGCTG 900
DB 871 GCCTTTCTGAGGAGGCGCCGGGAGAAACAGTCCCTATGAGCAGTGTGCTGCTGCTGCTG 930
QY 901 GAAGAAATCGCTGAGGAGGCTCAGAGACTCAGGCTCCAGGACTGGACATATCTGCACTC 960
DB 931 GAAGAAATCGCTGAGGAGGCTCAGAGACTCAGGCTCCAGGACTGGACATATCTGCACTC 990
QY 961 CTGCGCTCTGACTTACCGGCTACTTCCAAATATGAGGGGTCTCTGACTACACCGGCTGT 1020
DB 991 CTGCGCTCTGACTTACCGGCTACTTCCAAATATGAGGGGTCTCTGACTACACCGGCTGT 1050
QY 1021 GCCCAGGGTGTCTCTGAGCTGTGTTTAAACAGACAGTGTGCTGCTGCTGCTGCTGCTGCT 1080
DB 1051 GCCCAGGGTGTCTCTGAGCTGTGTTTAAACAGACAGTGTGCTGCTGCTGCTGCTGCTGCT 1110
QY 1081 CACACCCCTCTCTGACACCCCTGTGGGGACCTCGGTGACTCTCGGCTACAGCTGAACTTCGA 1140

Db 1111 CACACCTCTCTGACACCTCTGCGGACCTGCTGACTCTCGGCTACAGCTGAATCCGA 1170
Qy 1141 GCGAGCAGCCTTTGAATGGGCGAGTGATGAGGCTCTCCCTGCTGGAGTGACAGC 1200
Db 1171 GCGAGCAGCCTTTGAATGGGCGAGTGATGAGGCTCTCCCTGCTGGAGTGACAGC 1230
Qy 1201 AGTCTCTGGGCTGCTGAGCAGTCCAGCTGAATTCCTGCTGCTGGCTGCTGATCCTTA 1260
Db 1231 AGTCTCTGGGCTGCTGAGCAGTCCAGCTGAATTCCTGCTGCTGGCTGCTGATCCTTA 1290
Qy 1261 GCCCTGTTTGGCTCTCTTTTGTGTGTCAGAGCTGCTGCTCTCTTGTGAGATGAGA 1320
Db 1291 GCCCTGTTTGGCTCTCTTTTGTGTGTCAGAGCTGCTGCTCTCTTGTGAGATGAGA 1350
Qy 1321 AGGAGCAGCAGAGGGAACCAAGGGGTGTGAGTACCGCCAGCAGAGTACCGAG 1380
Db 1351 AGGAGCAGCAGAGGGAACCAAGGGGTGTGAGTACCGCCAGCAGAGTACCGAG 1410
Qy 1381 ACTGAGCCTAGAGGCTGGATCTTGAGAAATGTGAGAACTGAGAGCCAGAGGCACTGAGGG 1440
Db 1411 ACTGAGCCTAGAGGCTGGATCTTGAGAAATGTGAGAACTGAGAGCCAGAGGCACTGAGGG 1470
Qy 1441 GGAGCGGTAACTGCTCTGCTCTGCTCAATGATGCACTTTTAACTGCCAAGAAAT 1500
Db 1471 GGAGCGGTAACTGCTCTGCTCTGCTCAATGATGCACTTTTAACTGCCAAGAAAT 1530
Qy 1501 TTTTAAATAAATATTTAAT 1522
Db 1531 TTTTAAATAAATATTTAAT 1552

RESULT 6

ABL65416
ID ABL65416 standard; DNA; 1552 BP.

XX AC ABL65416;
XX DT 15-MAY-2002 (first entry)
XX DE Lung cancer related gene sequence SEQ ID NO:3753.
XX KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
XX KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
XX KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
XX KW gene; ds.
XX OS Homo sapiens.
XX PN WO200194629-A2.
XX PD 13-DEC-2001.
XX PF 30-MAY-2001; 2001WO-US010839.
XX PR 05-JUN-2000; 2000US-0209473P.
XX PR 05-JUN-2000; 2000US-0209531P.
XX PR 18-SEP-2000; 2000US-0233133P.
XX PR 18-SEP-2000; 2000US-0233617P.
XX PR 20-SEP-2000; 2000US-0234009P.
XX PR 20-SEP-2000; 2000US-0234034P.
XX PR 20-SEP-2000; 2000US-0234052P.
XX PR 22-SEP-2000; 2000US-0234509P.
XX PR 22-SEP-2000; 2000US-0234567P.
XX PR 25-SEP-2000; 2000US-0234923P.
XX PR 25-SEP-2000; 2000US-0234924P.
XX PR 25-SEP-2000; 2000US-0235077P.
XX PR 25-SEP-2000; 2000US-0235082P.
XX PR 25-SEP-2000; 2000US-0235134P.
XX PR 25-SEP-2000; 2000US-0235280P.
XX PR 26-SEP-2000; 2000US-0235637P.
XX PR 26-SEP-2000; 2000US-0235638P.
XX PR 27-SEP-2000; 2000US-0235711P.

PR 27-SEP-2000; 2000US-0235720P.
PR 27-SEP-2000; 2000US-0235840P.
PR 27-SEP-2000; 2000US-0235863P.
PR 28-SEP-2000; 2000US-0236028P.
PR 28-SEP-2000; 2000US-0236032P.
PR 28-SEP-2000; 2000US-0236033P.
PR 28-SEP-2000; 2000US-0236034P.
PR 28-SEP-2000; 2000US-0236109P.
PR 28-SEP-2000; 2000US-0236111P.
PR 28-SEP-2000; 2000US-0236842P.
PR 29-SEP-2000; 2000US-0236891P.
PR 02-OCT-2000; 2000US-0237172P.
PR 02-OCT-2000; 2000US-0237173P.
PR 02-OCT-2000; 2000US-0237278P.
PR 02-OCT-2000; 2000US-0237294P.
PR 02-OCT-2000; 2000US-0237295P.
PR 02-OCT-2000; 2000US-0237316P.
PR 03-OCT-2000; 2000US-0237425P.
PR 03-OCT-2000; 2000US-0237598P.
PR 03-OCT-2000; 2000US-0237604P.
PR 03-OCT-2000; 2000US-0237606P.
PR 03-OCT-2000; 2000US-0237608P.
PR 01-NOV-2000; 2000US-0244867P.
PR 01-NOV-2000; 2000US-0245084P.
PA (AVAL-) AVALON PHARM.
PI Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI Soppet DR, Weaver Z;
XX WPI; 2002-188264/24.
XX PT Screening for anti-neoplastic agent involves exposing cells to a chemical
PT agent to be tested for anti-neoplastic activity, and determining a change
PT in expression of a gene of a signature gene set.
XX Claim 1; SEQ ID NO 3753; 44pp; English.
XX The present invention describes a method (M1) for screening for an anti-
CC neoplastic agent. The method involves exposing cells to a chemical agent
CC to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (I) of a signature gene set, where (I)
CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC to ABL70110), or is at least 95% identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening an
CC anti-neoplastic agent, and can be used for producing a product which is
CC the data collected with respect to the anti-neoplastic agent as a result
CC of M1, and the data is sufficient to convey the chemical structure and/or
CC properties of the agent. M1 can be used in the treatment of cancer such
CC as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
CC cancer, infiltrating ductal cancer, neuroendocrine carcinoma, papillary cell
CC carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
CC tumour
SQ Sequence 1552 BP; 302 A; 471 C; 461 G; 318 T; 0 U; 0 Other;
Query Match 100.0%; Score 1522; DB 6; Length 1552;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ACAGTCAGCGCATGGCTCCCTGTGCCCCCAGCCCTCCCTCTCTGTGATCCCGCC 60
Db 31 ACAGTCAGCGCATGGCTCCCTGTGCCCCCAGCCCTCCCTCTCTGTGATCCCGCC 90
Qy 61 CTGCTCCAGGCTCACTGTGCAACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 120
Db 91 CTGCTCCAGGCTCACTGTGCAACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 150
Qy 121 CCCAGAGGTGGCCCCGATGAGGAGTATCCCCCTTTGGGAGGAGGCTCTTCTGGGAA 180
Db 151 CCCAGAGGTGGCCCCGATGAGGAGTATCCCCCTTTGGGAGGAGGCTCTTCTGGGAA 210

PR 02-OCT-2000; 2000US-0237172P.
PR 02-OCT-2000; 2000US-0237173P.
PR 02-OCT-2000; 2000US-0237278P.
PR 02-OCT-2000; 2000US-0237294P.
PR 02-OCT-2000; 2000US-0237295P.
PR 02-OCT-2000; 2000US-0237316P.
PR 03-OCT-2000; 2000US-0237425P.
PR 03-OCT-2000; 2000US-0237598P.
PR 03-OCT-2000; 2000US-0237604P.
PR 03-OCT-2000; 2000US-0237608P.
PR 03-OCT-2000; 2000US-0237609P.
PR 01-NOV-2000; 2000US-0244867P.
PR 01-NOV-2000; 2000US-0245084P.
XX
PA (AVAL-) AVALON PHARM.
XX
XX Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI Soppet DR, Weaver Z;
FI
XX
XX WPI; 2002-188264/24.
XX
XX Screening for anti-neoplastic agent involves exposing cells to a chemical
PT agent to be tested for anti-neoplastic activity, and determining a change
PT in expression of a gene of a signature gene set.
XX
XX
PS Claim 1; SEQ ID NO 6683; 44pp; English.
XX
XX The present invention describes a method (M1) for screening for an anti-
CC neoplastic agent. The method involves exposing cells to a chemical agent
CC to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (I) of a signature gene set, where (I)
CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC to ABL70110), or is at least 95% identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening an
CC anti-neoplastic agent, and can be used for producing a product which is
CC the data collected with respect to the anti-neoplastic agent as a result
CC of M1, and the data is sufficient to convey the chemical structure and/or
CC properties of the agent. M1 can be used in the treatment of cancer such
CC as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
CC cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilms
CC tumour
XX
XX Sequence 1552 BP; 302 A; 471 C; 461 G; 318 T; 0 U; 0 Other;
Query Match 100.0%; Score 1522; DB 6; Length 1552;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACAGTCAGCGGATGGCTCCCTGTCGCCAGCCCTGGCTCCCTCTGTTGATCCGGCC 60
DB 31 ACAGTCAGCGGATGGCTCCCTGTCGCCAGCCCTGGCTCCCTCTGTTGATCCGGCC 90
QY 61 CTTGCTCAGGCTCAGTGTGCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
DB 91 CTTGCTCAGGCTCAGTGTGCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 150
QY 121 CCCCAGAGGTTGCCCGGATGAGGAGGATTCCTCCCTTGGGAGGAGGCTCTTCTGGGAA 180
DB 151 CCCCAGAGGTTGCCCGGATGAGGAGGATTCCTCCCTTGGGAGGAGGCTCTTCTGGGAA 210
QY 181 GATGACCACTGGGAGGAGGATCTGCCAGTGAAGAGGATTCACCCAGAGAGGAGAT 240
DB 211 GATGACCACTGGGAGGAGGATCTGCCAGTGAAGAGGATTCACCCAGAGAGGAGAT 270
QY 241 CCACCCGGAGGAGGATCTACTCGAGAGGAGGATCTACTCGAGAGGAGGATCTACT 300
DB 271 CCACCCGGAGGAGGATCTACTCGAGAGGAGGATCTACTCGAGAGGAGGATCTACT 330
QY 301 GAAGTTAAGCCTAAATCAGAAAGAGGGCTCCCTGAAAGTTAGAGGATCTACTACTGTT 360
DB

DB 331 GAAGTTAAGCCTAAATCAGAAAGAGGGCTCCCTGAAAGTTAGAGGATCTACTACTGTT 390
QY 361 GAGGCTCCTGGAGATCCTCAAGAACCCAGAAATATGCCACAGGACAAAGAGAGGGAT 420
DB 391 GAGGCTCCTGGAGATCCTCAAGAAACCCAGAAATATGCCACAGGACAAAGAGAGGGAT 450
QY 421 GACCAGAGTCAATTTGGCGCTATGAGGAGGACCCCGCCCTGGCCCGGGGTGTCCTCCAGCCTGC 480
DB 451 GACCAGAGTCAATTTGGCGCTATGAGGAGGACCCCGCCCTGGCCCGGGGTGTCCTCCAGCCTGC 510
QY 481 GCGGGCGCTTCCAGTCCCGGTGGATATCCGCCCCAGCTGCGCGCTTCTGCGCCGCC 540
DB 511 GCGGGCGCTTCCAGTCCCGGTGGATATCCGCCCCAGCTGCGCGCTTCTGCGCCGCC 570
QY 541 CTGGCCCGCTTGGAACTCCAGCTCCCGCGCTCCAGAACTCCAGAACTCCAGAACTCCAG 600
DB 571 CTGGCCCGCTTGGAACTCCAGCTCCCGCGCTCCAGAACTCCAGAACTCCAGAACTCCAG 630
QY 601 AACAAATGCCACAGTGTGCAACTGACCTGCTCTGCGCTTAGAGATGGCTCTGGGTCCC 660
DB 631 AACAAATGCCACAGTGTGCAACTGACCTGCTCTGCGCTTAGAGATGGCTCTGGGTCCC 690
QY 661 GGGCGGAGTACCGGGCTCTGCACTGCACTGCGGGGGCTGCAAGTCTGTCGGGC 720
DB 691 GGGCGGAGTACCGGGCTCTGCACTGCACTGCGGGGGCTGCAAGTCTGTCGGGC 750
QY 721 TCGGAGCACACTGTTGAGGCGCCCGTTTCCCTCCCGAGATCCAGTGGTTCACCTCAGC 780
DB 751 TCGGAGCACACTGTTGAGGCGCCCGTTTCCCTCCCGAGATCCAGTGGTTCACCTCAGC 810
QY 781 ACCGCTTTGCGAGAGGCTGAGGCGCTTGGGGGGCCCGGAGGCTTGGCGGTGTTGGCC 840
DB 811 ACCGCTTTGCGAGAGGCTGAGGCGCTTGGGGGGCCCGGAGGCTTGGCGGTGTTGGCC 870
QY 841 GCCTTTTGGAGAGGCGCCCGGAAAGAAAGAGTGCCTATGAGAGTGTCTGCTGCTG 900
DB 871 GCCTTTTGGAGAGGCGCCCGGAAAGAAAGAGTGCCTATGAGAGTGTCTGCTGCTG 930
QY 901 GAAGAAATCGCTGAGGAGGCTCAGAGACTCAGAGTCCAGGACTGGACATATGCACTC 960
DB 931 GAAGAAATCGCTGAGGAGGCTCAGAGACTCAGAGTCCAGGACTGGACATATGCACTC 990
QY 961 CTGCGCTCTGACTTTCAGCGCTTCTCCAATATGAGGGGTCTCTGACTACACCGCGCTG 1020
DB 991 CTGCGCTCTGACTTTCAGCGCTTCTCCAATATGAGGGGTCTCTGACTACACCGCGCTG 1050
QY 1021 GCCCAGGGTGTCTGGAATGTTTAAACAGAGAGTGTGCTGCTGCTGCTGCTGCTGCTG 1080
DB 1051 GCCCAGGGTGTCTGGAATGTTTAAACAGAGAGTGTGCTGCTGCTGCTGCTGCTGCTG 1110
QY 1081 CACACCTCTCTGACACCCCTGTTGGGACCTGTTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
DB 1111 CACACCTCTCTGACACCCCTGTTGGGACCTGTTGCTGCTGCTGCTGCTGCTGCTGCTG 1170
QY 1141 CCGACGAGCCTTTGAATGGCGGAGTGAATGAGGCTCTCTTCCCTGCTGCTGCTGCTGCTG 1200
DB 1171 CCGACGAGCCTTTGAATGGCGGAGTGAATGAGGCTCTCTTCCCTGCTGCTGCTGCTGCTG 1230
QY 1201 AGTCTCTGGGTGCTGAGCCAGTCCAGCTGAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260
DB 1231 AGTCTCTGGGTGCTGAGCCAGTCCAGCTGAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTG 1290
QY 1261 GCCCTGTTTGGCTCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320
DB 1291 GCCCTGTTTGGCTCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1350
QY 1321 AGGACGACACAGAGGGGAAACCAAGGGGGTGTGAGCTACCCGCCAGAGAGGTAGCCGAG 1380
DB 1351 AGGACGACACAGAGGGGAAACCAAGGGGGTGTGAGCTACCCGCCAGAGAGGTAGCCGAG 1410
QY 1381 ACTGAGCCTAGAGGCTGGATCTTGGAGAAATGTGAGAAAGCCAGCCAGAGGATCTGAGGG 1440
DB 1411 ACTGAGCCTAGAGGCTGGATCTTGGAGAAATGTGAGAAAGCCAGCCAGAGGATCTGAGGG 1470

Db 691 GGGCGGAGTACCGGCTCTGCGAGCTGTCATCTGCACTGGGGGCTGCGAGTGTGCGGGC 750
Qy 721 TCGGAGCACACTGTGAGAGCCACCGTTTCCCTGCCGAGATCCACGTGTTTCACTCAGC 780
Db 751 TCGGAGCACACTGTGAGAGCCACCGTTTCCCTGCCGAGATCCACGTGTTTCACTCAGC 810
Qy 781 ACCGCTTTTCCAGAGTTGACGAGGCTTGGGGCCCGGGAGGCTTGGGCGGTGGCC 840
Db 811 ACCGCTTTTCCAGAGTTGACGAGGCTTGGGGCCCGGGAGGCTTGGGCGGTGGCC 870
Qy 841 GCCTTTTCCAGAGGCGCCGAGAAACAGTGCCTTATGAGCAGTTGCTGTCTCGCTTG 900
Db 871 GCCTTTTCCAGAGGCGCCGAGAAACAGTGCCTTATGAGCAGTTGCTGTCTCGCTTG 930
Qy 901 GAGAAATCGCTGAGGAGCTCAGACACTCAGTCCAGGACTGGACATATCTGCACTC 960
Db 931 GAGAAATCGCTGAGGAGCTCAGACACTCAGTCCAGGACTGGACATATCTGCACTC 990
Qy 961 CTGCTCTCAGCTTTCAGCGCTACTTCCAATATGAGGCTCTCTGACTACACGCGCTGT 1020
Db 991 CTGCTCTCAGCTTTCAGCGCTACTTCCAATATGAGGCTCTCTGACTACACGCGCTGT 1050
Qy 1021 GCCAGGCTCTCATCTGAGCTGTGTTTAAACAGACAGTGTGCTGCTGTAAGCAGCTC 1080
Db 1051 GCCAGGCTCTCATCTGAGCTGTGTTTAAACAGACAGTGTGCTGCTGTAAGCAGCTC 1110
Qy 1081 CACACCTCTCTGACACCTCTGTGGGACCTGTGTGACTCTCGGTAAGTGTGTAATCCGA 1140
Db 1111 CACACCTCTCTGACACCTCTGTGGGACCTGTGTGACTCTCGGTAAGTGTGTAATCCGA 1170
Qy 1141 GCGACGAGCTTTGAATGGCGAGTGATTTGAGGCTCTTCCCTGCTGAGTGAGCAGC 1200
Db 1171 GCGACGAGCTTTGAATGGCGAGTGATTTGAGGCTCTTCCCTGCTGAGTGAGCAGC 1230
Qy 1201 AGTCTCGGCTGTGAGCAGCTCAGCTGAATTTCTGCTGCTGCTGCTGCTGCTGCTA 1260
Db 1231 AGTCTCGGCTGTGAGCAGCTCAGCTGAATTTCTGCTGCTGCTGCTGCTGCTGCTA 1290
Qy 1261 GCCTGTGTTTGGCTCTCTTTTGTGTCACAGCTGCTGCTGCTGCTGCTGCTGCTGCTA 1320
Db 1291 GCCTGTGTTTGGCTCTCTTTTGTGTCACAGCTGCTGCTGCTGCTGCTGCTGCTGCTA 1350
Qy 1321 AGCAGCAGAGAGGAGAACCAAGGGGTGTGAGCTTACCGCCAGCAGAGTACCGAG 1380
Db 1351 AGCAGCAGAGAGGAGAACCAAGGGGTGTGAGCTTACCGCCAGCAGAGTACCGAG 1410
Qy 1381 ACTGAGCCTTAGAGGCTTGGATCTTGGAGATGTGAGAGCCAGCAGGCACTCTGAGG 1440
Db 1411 ACTGAGCCTTAGAGGCTTGGATCTTGGAGATGTGAGAGCCAGCAGGCACTCTGAGG 1470
Qy 1441 GGAGCGGTAACTGTCTGTCTGCTCATTAATGCACTTCTTTTAACTGCCAAGAAAT 1500
Db 1471 GGAGCGGTAACTGTCTGTCTGCTCATTAATGCACTTCTTTTAACTGCCAAGAAAT 1530
Qy 1501 TTTTAAATAAATAATTTATTAAT 1522
Db 1531 TTTTAAATAAATAATTTATTAAT 1552

RESULT 10

ABX76385
ID ABX76385 standard; DNA; 1552 BP.
XX
XX AC ABX76385;
XX
DT 02-APR-2003 (first entry)
XX
DE Lung cancer-associated polynucleotide #249.

XX Lung cancer-associated polynucleotide; gene; ds; cytostatic; emphysema;
KW antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;
KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;

KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
XX Unidentified.
XX WO200286443-A2.
XX 31-OCT-2002.
PD 18-APR-2002; 2002WO-US012476.
XX 18-APR-2001; 2001US-0284770P.
PR 10-MAY-2001; 2001US-0290492P.
PR 09-NOV-2001; 2001US-0339245P.
PR 13-NOV-2001; 2001US-0350666P.
PR 23-NOV-2001; 2001US-0334370P.
PR 12-APR-2002; 2002US-0372246P.
XX (EOSB-) EOS BIOTECHNOLOGY INC.

Aziz N, Murray R;

WPI; 2003-093161/08.

P-PSDB; ABUS6656.

Detecting a lung cancer-associated transcript in a cell from a patient for treating lung cancer, by contacting a biological sample from the patient with a polynucleotide that exhibits increased or decreased expression in lung cancer.

Claim 22; Page 379-380; 453pp; English.

The invention relates to a method for detecting a lung cancer-associated transcript in a cell from a patient, comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridises to a sequence that is at least 80 % identical to a gene that exhibits increased or decreased expression in lung cancer samples. Lung cancer-associated polynucleotides and polypeptides are used for identifying a compound that modulates a lung cancer-associated polypeptide, for inhibiting proliferation of a lung cancer-associated cell to treat lung cancer in a patient and for treating a mammal having lung cancer by administering a modulatory compound identified. The methods are useful for treating lung cancer, such as small cell lung cancer, non-small cell lung cancer or other benign or precancerous lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and bronchiectasis. The genes, polynucleotides and polypeptides are useful for diagnostic purposes and as targets for screening for therapeutic compounds that modulate lung cancer, such as antibodies. Sequences ABX76124-ABX76474 represent lung cancer-associated polynucleotides of the invention

Sequence 1552 BP; 302 A; 471 C; 461 G; 318 T; 0 U; 0 Other;

Query Match 100.0%; Score 1522; DB 7; Length 1552;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACAGTCAGCGCAGTGTCCCTGTGCCCCAGCCCTCGCTCCCTCTGTGATCCCCGCC 60

Db 31 ACAGTCAGCGCAGTGTCCCTGTGCCCCAGCCCTCGCTCCCTCTGTGATCCCCGCC 90

Qy 61 CTGTCTCCAGGCTCTACTGTGCACTGTCTGTCTGTCTGTCTGTCTGTCTGTCTCAT 120

Db 91 CTGTCTCCAGGCTCTACTGTGCACTGTCTGTCTGTCTGTCTGTCTGTCTGTCTCAT 150

Qy 121 CCCAGAGGTTGCCCGGATGTCAGGAGGATTCCTCCCTTGGGAGAGGCTCTTCTGGGGAA 180

Db 151 CCCAGAGGTTGCCCGGATGTCAGGAGGATTCCTCCCTTGGGAGAGGCTCTTCTGGGGAA 210

Qy 181 GATGACCCACTGGCGGAGGAGGATTCGCCAGTGAAGAGATTCACCCAGAGAGGAGAT 240

Db 211 GATGACCCACTGGCGGAGGAGGATTCGCCAGTGAAGAGATTCACCCAGAGAGGAGAT 270

lung cancer or other benign or precancerous lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and bronchiectasis. The genes, polynucleotides and polypeptides are useful for diagnostic purposes and as targets for screening for therapeutic compounds that modulate lung cancer, such as antibodies. Sequences ABX76124-ABX76474 represent lung cancer-associated polynucleotides of the invention

SQ Sequence 1552 BP; 302 A; 471 C; 461 G; 318 T; 0 U; 0 Other;

Query Match 100.0%; Score 1522; DB 7; Length 1552;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0;

| | | | | | | |
|-----|----|---|------|--|---|-----|
| 1 | QY | A | CAGT | CAGCGCAT | TGGCTCCCTGTGCCCCAGCCCCCTGGCTCCCTCTGTTGATCCCGGCC | 60 |
| 31 | DB | A | CAGT | CAGCGCAT | TGGCTCCCTGTGCCCCAGCCCCCTGGCTCCCTCTGTTGATCCCGGCC | 90 |
| 61 | QY | C | TGCT | CCAGGCTC | CACATGCTGCTGTCACTGCTGCTTCTGATGCCCTGTCCAT | 120 |
| 91 | DB | C | TGCT | CCAGGCTC | CACATGCTGCTGTCACTGCTGCTTCTGATGCCCTGTCCAT | 150 |
| 121 | QY | C | CC | CAGAGT | TGCCCCCGGATCGAGAGGATTCGCCCTTGGAGGAGGCTCTTCTGGGGAA | 180 |
| 151 | DB | C | CC | CAGAGT | TGCCCCCGGATCGAGAGGATTCGCCCTTGGAGGAGGCTCTTCTGGGGAA | 210 |
| 181 | QY | G | ATG | ACCACT | TGGCGAGGAGGATCTGCCAGTGAAGAGATTCA | 240 |
| 211 | DB | G | ATG | ACCACT | TGGCGAGGAGGATCTGCCAGTGAAGAGATTCA | 270 |
| 241 | QY | C | CA | CCCGGAGAGGAGGATCTACCTGGAGAGAGGATCTACCTGGAGAGGAGGATCTACCT | 300 | |
| 271 | DB | C | CA | CCCGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT | 330 | |
| 301 | QY | G | AA | GTTAAGCCT | TAATCAGAAGAAGAGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT | 360 |
| 331 | DB | G | AA | GTTAAGCCT | TAATCAGAAGAAGAGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT | 390 |
| 361 | QY | G | AGG | CTCCTGGAGATCTCTCAAGAACCCAGAAATAATGCCCCACAGGAGNACAAGAGGGAT | 420 | |
| 391 | DB | G | AGG | CTCCTGGAGATCTCTCAAGAACCCAGAAATAATGCCCCACAGGAGNACAAGAGGGAT | 450 | |
| 421 | QY | G | ACC | CAGAGTCA | TGCGCGCTATGGAGGGGACCCCGCCCTGGCCCCCGGGTGTCGCCAGGCTCG | 480 |
| 451 | DB | G | ACC | CAGAGTCA | TGCGCGCTATGGAGGGGACCCCGCCCTGGCCCCCGGGTGTCGCCAGGCTCG | 510 |
| 481 | QY | G | CG | CGCGCTTCCAGTCCCGGTGGATATCGCGCCCCCAGCTCGCGCTTCTGCCCCGGCC | 540 | |
| 511 | DB | G | CG | CGCGCTTCCAGTCCCGGTGGATATCGCGCCCCCAGCTCGCGCTTCTGCCCCGGCC | 570 | |
| 541 | QY | C | TG | CGCCCCCTGGAACTCTCTGGCTTCAGGCTCCGCGCGCTCCAGAACTGCGGCTGCGC | 600 | |
| 571 | DB | C | TG | CGCCCCCTGGAACTCTCTGGCTTCAGGCTCCGCGCGCTCCAGAACTGCGGCTGCGC | 630 | |
| 601 | QY | A | ACA | TGSCACAGTGTCAACTGACCTGCTCCTGSGGCTAGAGATGGCTCTGGGTCCC | 660 | |
| 631 | DB | A | ACA | TGSCACAGTGTCAACTGACCTGCTCCTGSGGCTAGAGATGGCTCTGGGTCCC | 690 | |
| 661 | QY | G | GG | CGGGAGTACCGGGCTCTCGAGCTGCATCTGCACTGGGGGGCTGCAAGTCTGCGGGC | 720 | |
| 691 | DB | G | GG | CGGGAGTACCGGGCTCTCGAGCTGCATCTGCACTGGGGGGCTGCAAGTCTGCGGGC | 750 | |
| 721 | QY | T | CG | GAGCACACTGTGGAAGGCCACGGTTTCCCTGCCGAGATCA | 780 | |
| 751 | DB | T | CG | GAGCACACTGTGGAAGGCCACGGTTTCCCTGCCGAGATCA | 810 | |
| 781 | QY | A | CC | CGCTTTGCCAGAGTTGACAGGCGCTTGGGGGGCCCCGGAGGCTCTGGCGGTGTTGGCC | 840 | |
| 811 | DB | A | CC | CGCTTTGCCAGAGTTGACAGGCGCTTGGGGGGCCCCGGAGGCTCTGGCGGTGTTGGCC | 870 | |
| 841 | QY | G | CT | TTCTGGAGGGGCCCGCGAAACAGTGCCTTATGAGCAGTTGTGTCTCGCTTG | 900 | |

XX 23-AUG-2001.
XX PD
XX PF 13-FEB-2001; 2001WO-US004595.
XX PR 14-FEB-2000; 2000US-0182429P.
XX PR 15-FEB-2000; 2000US-0182636P.
XX PA (REGC) UNIV CALIFORNIA.
XX PI Belidegrun A, Tso C;
XX DR WPI; 2001-557625/62.
XX DR P-PSDB; AAB82848.
PT New construct with a G250 kidney cancer specific antigen attached to a
PT granulocyte macrophage colony stimulating factor, useful in gene therapy
PT or as a vaccine for treating renal cell cancers.
XX Claim 24; Page 76; 78pp; English.
XX CC The present sequence is that of a nucleic acid encoding a fusion protein
CC (see AAB82848) composed of the G250 kidney cancer specific antigen
CC attached via a dipeptide linker to human granulocyte macrophage colony
CC stimulating factor (GM-CSF). The construct was produced by ligation of
CC full-length human GM-CSF cDNA from plasmid p91023(B) and full-length G250
CC cDNA obtained by PCR amplification. The resulting fusion gene was
CC inserted into a baculovirus vector for fusion protein production in Sf98
CC insect cells. The fusion protein raises an immune response directed
CC against renal cell cancers. It can be used as a vaccine or in adoptive
CC immunotherapy. Nucleic acids encoding the fusion protein can be used as
CC DNA vaccines, to transfect cells in an adoptive immunotherapy treatment
CC regimen, and in gene therapy for treating or preventing renal cell
XX cancers
SQ Sequence 1833 BP; 357 A; 571 C; 543 G; 362 T; 0 U; 0 Other;
Query Match 90.7%; Score 1379.8; DB 4; Length 1833;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1381; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 16 GTCCTCCCTGTGCCCCAGCCCTGCTCCCTCTGTTGATCCCGGCCCTCTCCAGGCCTC 75
DB 439 GCTCCCTGTGCCCCAGCCCTGCTCCCTCTGTTGATCCCGGCCCTCTCCAGGCCTC 498
QY 76 ACTGTCAACTGCTGTCTGCTCACTGCTCTCTGATGCTGCTCCATCCCGAGGTTGCC 135
DB 499 ACTGTCAACTGCTGTCTGCTCACTGCTCTCTGATGCTGCTCCATCCCGAGGTTGCC 558
QY 136 CGGATCGAGGAGGATTCCTCCCTTGGGAGGAGGCTCTTCTGGGAGAGATGACCCACTGGGC 195
DB 559 CGGATCGAGGAGGATTCCTCCCTTGGGAGGAGGCTCTTCTGGGAGAGATGACCCACTGGGC 618
QY 196 GAGGAGGATCTGCCAGTGAAGAGGATTCACCCAGAGAGAGGATCCACCCGAGAGGAG 255
DB 619 GAGGAGGATCTGCCAGTGAAGAGGATTCACCCAGAGAGAGGATCCACCCGAGAGGAG 678
QY 256 GATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGAAGTTAAGCCTAAA 315
DB 679 GATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGAAGTTAAGCCTAAA 738
QY 316 TCAGAGAGAGAGGAGGCTCCCTGAAGTTAGAGGATCTACCTACTGTTGAGGCTCTCTGAGAT 375
DB 739 TCAGAGAGAGAGGAGGCTCCCTGAAGTTAGAGGATCTACCTACTGTTGAGGCTCTCTGAGAT 798
QY 376 CCTCAAGAACCCCGAGAGATTAATGCCCAAGAGGAGGAGATCAACAGAGTCAATTGG 435
DB 799 CCTCAAGAACCCCGAGAGATTAATGCCCAAGAGGAGGAGATCAACAGAGTCAATTGG 858
QY 436 CGCTATGGAGGAGAGCCCGCCCTGGCCCGCGGGTGTCCCCAGCCTGCGCGGCGCTTCCAG 495
DB 859 CGCTATGGAGGAGAGCCCGCCCTGGCCCGCGGGTGTCCCCAGCCTGCGCGGCGCTTCCAG 918

QY 496 TCCCGGTGGATATCCGCCCCCGAGCTCCGCGCTTCTGCCCCGGCCCTGCGCCCCCTGGAA 555
DB 919 TCCCGGTGGATATCCGCCCCCGAGCTCCGCGCTTCTGCCCCGGCCCTGCGCCCCCTGGAA 978
QY 556 CTCCTGGGCTTCCAGCTCCCGCGCTCCAGAACTGCGGCTTCGCGCAACATGCGCCACAGT 615
DB 979 CTCCTGGGCTTCCAGCTCCCGCGCTCCAGAACTGCGGCTTCGCGCAACATGCGCCACAGT 1038
QY 616 GTGCAACTGACCCCTGCTGGGCTAGAGATGGCTCTGGGTCCCGGGGGAGTACCGG 675
DB 1039 GTGCAACTGACCCCTGCTGGGCTAGAGATGGCTCTGGGTCCCGGGGGAGTACCGG 1098
QY 676 GCTCTGCAGCTGCATCTGCACTGGGGGCTGCAGTCTGTCGGGCTCGGAGCACACTGTG 735
DB 1099 GCTCTGCAGCTGCATCTGCACTGGGGGCTGCAGTCTGTCGGGCTCGGAGCACACTGTG 1158
QY 736 GAAGGCCACCGTTTCCCTGCGGAGATCCAGTGGTTTCACTCAGCACCGCTTTGCCAGA 795
DB 1159 GAAGGCCACCGTTTCCCTGCGGAGATCCAGTGGTTTCACTCAGCACCGCTTTGCCAGA 1218
QY 796 GTTGACGAGGCTTGGGGCGCCCGGAGGCTTGGCGCTGTTGGCGCCCTTCTTGAGGAG 855
DB 1219 GTTGACGAGGCTTGGGGCGCCCGGAGGCTTGGCGCTGTTGGCGCCCTTCTTGAGGAG 1278
QY 856 GGCCCGGAGAAACAGTGCCTTATGAGCAGTTGTCTCTCGCTTGGAAAGAAATCGCTGAG 915
DB 1279 GGCCCGGAGAAACAGTGCCTTATGAGCAGTTGTCTCTCGCTTGGAAAGAAATCGCTGAG 1338
QY 916 GAAGCTCAGAGACTCAGGTGCCAGACTGGACATATCTGCACTCTGCGCCCTTGCATTC 975
DB 1339 GAAGCTCAGAGACTCAGGTGCCAGACTGGACATATCTGCACTCTGCGCCCTTGCATTC 1398
QY 976 AGCCCTACTTCCAAATATAGGGGCTCTGACTACACCGCCCTGTGCCAGGGTGTCACTC 1035
DB 1399 AGCCCTACTTCCAAATATAGGGGCTCTGACTACACCGCCCTGTGCCAGGGTGTCACTC 1458
QY 1036 TGGACTGTGTTTAAACAGACAGTGAATGCTGAAGTGTAAAGAGCTCCACACCTCTCTGAC 1095
DB 1459 TGGACTGTGTTTAAACAGACAGTGAATGCTGAAGTGTAAAGAGCTCCACACCTCTCTGAC 1518
QY 1096 ACCCTGTGGGACCTGGTGACTCTCGGCTACAGCTGAACTTCCGAGCGACGAGCCTTTG 1155
DB 1519 ACCCTGTGGGACCTGGTGACTCTCGGCTACAGCTGAACTTCCGAGCGACGAGCCTTTG 1578
QY 1156 AATGGCGCAGTGAATGAGGCTCTTCTCTGCTGAGTGGAGCAGAGTCTCTCGGCTGCT 1215
DB 1579 AATGGCGCAGTGAATGAGGCTCTTCTCTGCTGAGTGGAGCAGAGTCTCTCGGCTGCT 1638
QY 1216 GAGCCAGTCCAGTGAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1275
DB 1639 GAGCCAGTCCAGTGAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1698
QY 1276 CTCCTTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1335
DB 1699 CTCCTTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1758
QY 1336 GGAAACCAAGGGGCTGCTGAGTACCGCCAGCAGAGTGTAGCCGAGACTGGAGCTAGAGG 1395
DB 1759 GGAAACCAAGGGGCTGCTGAGTACCGCCAGCAGAGTGTAGCCGAGACTGGAGCTAGAGG 1818
QY 1396 CTG 1398
DB 1819 GTG 1821

RESULT 13
AAQ48456
ID AAQ48456 standard; cdna; 1397 BP.
XX
AC AAQ48456;
XX 25-MAR-2003 (revised)
DT 25-MAR-1994 (first entry)

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 11, 2004, 12:29:03 ; Search time 4181 seconds
(without alignments)
10870.662 Million cell updates/sec

Title: US-09-807-949b-1

Perfect score: 1522

Sequence: 1 acagtcagcgcgcatggtcc.....ttaataataattattataat 1522

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST.*

1: em_estba.*

2: em_esthum.*

3: em_estin.*

4: em_estmu.*

5: em_estov.*

6: em_estpl.*

7: em_estro.*

8: em_estc.*

9: gb_estl.*

10: gb_est2.*

11: gb_est3.*

12: gb_est4.*

13: gb_est5.*

14: gb_est6.*

15: em_estfun.*

16: em_estom.*

17: em_gss_hum.*

18: em_gss_inv.*

19: em_gss_pln.*

20: em_gss_vrt.*

21: em_gss_fun.*

22: em_gss_mam.*

23: em_gss_mus.*

24: em_gss_pro.*

25: em_gss_rod.*

26: em_gss_phg.*

27: em_gss_vri.*

28: gb_gss1.*

29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | ID | Description |
|------------|--------|---------------|--------|----|-------------|
| 1 | 1053.8 | 69.2 | 1201 | 9 | AL542336 |
| 2 | 920.8 | 60.5 | 1201 | 9 | AL554705 |
| 3 | 915 | 60.1 | 1013 | 13 | BX423970 |
| 4 | 903.4 | 59.4 | 1072 | 9 | AL558378 |

| | | | | | | |
|---|----|-------|------|------|----|--------------------|
| C | 5 | 865.2 | 56.8 | 1201 | 9 | AL554665 |
| C | 6 | 832 | 54.7 | 1201 | 13 | BX401186 |
| C | 7 | 813.6 | 53.5 | 1007 | 13 | BX423969 |
| C | 8 | 796.8 | 52.4 | 1031 | 9 | AL577748 |
| C | 9 | 789.4 | 51.9 | 1017 | 9 | AL580216 |
| C | 10 | 772.6 | 50.8 | 1067 | 9 | AL555184 |
| C | 11 | 731.4 | 48.1 | 874 | 12 | BG386425 |
| C | 12 | 669.8 | 44.0 | 689 | 14 | CA25935 UI-H-PE1- |
| C | 13 | 665.8 | 43.7 | 682 | 9 | AI831707 wj40h01.x |
| C | 14 | 665.4 | 43.4 | 1074 | 13 | BX383092 |
| C | 15 | 660.4 | 42.7 | 691 | 13 | BX620600 |
| C | 16 | 650.6 | 42.7 | 795 | 9 | AW083555 xc14903.x |
| C | 17 | 647 | 42.5 | 669 | 9 | AI925646 |
| C | 18 | 644 | 42.3 | 668 | 12 | BG824243 |
| C | 19 | 629.2 | 41.3 | 733 | 12 | BG819731 |
| C | 20 | 627.8 | 41.2 | 658 | 9 | AI769526 wj24a11.x |
| C | 21 | 625.6 | 41.1 | 818 | 10 | BE548062 |
| C | 22 | 620.8 | 40.8 | 806 | 10 | BF344769 |
| C | 23 | 608.4 | 40.0 | 659 | 14 | CA416326 UI-H-PEO- |
| C | 24 | 586.4 | 38.5 | 589 | 12 | BM790508 |
| C | 25 | 582.2 | 38.3 | 618 | 10 | AW615291 |
| C | 26 | 575.6 | 37.8 | 814 | 9 | AI241681 |
| C | 27 | 572 | 37.6 | 627 | 12 | BM552941 |
| C | 28 | 569.8 | 37.4 | 746 | 12 | BI223232 |
| C | 29 | 564 | 37.1 | 577 | 9 | AI032380 |
| C | 30 | 541.6 | 35.6 | 736 | 10 | BE543633 |
| C | 31 | 522.6 | 34.3 | 581 | 9 | AI023541 |
| C | 32 | 514.6 | 33.8 | 543 | 9 | AA879425 |
| C | 33 | 512 | 33.6 | 579 | 9 | AI400286 |
| C | 34 | 501.2 | 32.9 | 525 | 9 | AI979142 |
| C | 35 | 495.8 | 32.6 | 551 | 14 | CA406362 |
| C | 36 | 489 | 32.1 | 489 | 9 | AI791726 |
| C | 37 | 488.2 | 32.1 | 969 | 13 | BX370540 |
| C | 38 | 474.2 | 31.2 | 945 | 14 | CF579370 |
| C | 39 | 465.2 | 30.6 | 717 | 10 | AW701559 |
| C | 40 | 461 | 30.3 | 541 | 12 | BM792326 |
| C | 41 | 456.8 | 30.0 | 597 | 12 | BG746869 |
| C | 42 | 450.8 | 29.6 | 649 | 13 | BY735107 |
| C | 43 | 448.6 | 29.5 | 610 | 14 | CF177855 |
| C | 44 | 447.8 | 29.4 | 465 | 10 | AW293135 |
| C | 45 | 424 | 27.9 | 438 | 10 | AW449513 |

ALIGNMENTS

RESULT 1

AL542336

LOCUS

DEFINITION

5-PRIME, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AL542336 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE010YB19
1201 bp mRNA linear EST 12-MAY-2003
AL542336 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE010YB19
5-PRIME, mRNA sequence.
AL542336
AL542336.2 GI:30547384
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:12874280.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 8734.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DE010CA10QP2&cluster=8734.f. Contact :
Peng Liang Email : fliang@lifetech.com URL :


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Qy 901 GAAGAAATCGCTGAGGAGGCTCAGAGACTCAGGTCCAGGACTGGACATATCGCACTC 960
Db 992 GAA-RAATCGCTGAGGAA-GCTCAGAGACTCAGGKCCAGGACTGGACAWAT-TGCATC 1048
Qy 961 CTGCC 965
Db 1049 CTGCC 1053

RESULT 5
AL554665/c
LOCUS
DEFINITION
AL554665 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
AL554665
ACCESSION
VERSION
KEYWORDS
SOURCE
EST.
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:12895665.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5300.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DI085DC09NP1&cluster=5300.f. Contact :
Peng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DI085DC09NP1.
Location/Qualifiers
1. 1201
/organism="Homo sapiens"
/mol_type="mRNA"
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/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="First strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

FEATURES
source
Query Match 56.8%; Score 865.2; DB 9; Length 1201;
Best Local Similarity 92.0%; Pred. No. 4.6e-182;
Matches 1027; Conservative 23; Mismatches 47; Indels 19; Gaps 13;

Qy 407 ACAAGAAGGGGATGACAGAGTCAATGGCGCTATGAGGCGACCGCCCTGGCCCCCGGG 466
Db 1108 AGAAAAAARGGGATACCAATTAATTTGGCTATGAAGGC--ACCGCCCTTGGCCCGG 1051

Qy 467 TGTCCTCCAGCTCGCGGGCGCTCCAGTCCCGGTGGATATCCGCCCGCTCCCG 526
Db 1050 TGTCCTCCAGCTCGCGC-GGCGCTHGMAGTCCCGGT-GATATCCGCCCGCG-TYCCG 994

Qy 527 CTTCTCGCCCGCTGGCCCGCTCGGAACCTCTGGGCTTCAGCTCCCGCGCTCCAG 586
Db 993 CTTCTCGCCCG-CCYGGCCCTTGA--CTCCTGSGTTCVGVSTCCSCCGTCCAG 937

Qy 587 AACTGCGCTCGCAACAATGGCCACAGTGTGCACTGACCTCGCTCTGGGTAGAGA 646
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Qy 647 TGGCTCTGGTCCCGGCGGAGTACCGGGCTCTGCAGCTGCATCTGCACCTGGGGGCTG 706
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Qy 707 CAGGTCTGGTCCGGGCTCGGAGCACACTGTGTGAAGGCCACCGTTTCCCTTCCGAGATCCAG 766
Db 817 CAGGTCTGGTCCGGGCTCGGAGCACACTGTGTGAAGGCCACCGTTTCCCTTCCGAGATCCAG 758
Qy 767 TGGTTCACTCAGCACCGCTTTCAGAGAGTTCAGGAGGCTTGGGGGCGCCCGGAGGCC 826
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Qy 827 TGGCCGTGTTGGCGGCTTTCAGAGAGGCGCCCGGAAGAAAACAGTGCCTATCAGCAGT 886
Db 697 TGGCCGTGTTGGCGGCTTTCAGAGAGGCGCCCGGAAGAAAACAGTGCCTATCAGCAGT 638
Qy 887 TGTCTCTCGCTTGGAGAAATCGCTGAGAGAGGCTCAGAGACTCAGGTCCCAGGACT-- 944
Db 637 GGTCTCTCGCTTGGAGAAATCGCTGAGAGAGGCTCAGAGACTCAGGTCCCAGGACTCG 578
Qy 945 GGACATATCTGCACCTCT--GCCCTCTGACTTTCAGCGG--CTACTTCCAATATGAGGGCTCT 1002
Db 577 CGACATCTCTGCACCTCTCTCGCCCTCTCAGTTCAGCGGCCCTTCCAATATGAGGGGCTCT 518
Qy 1003 CTGACTACACCGCCCTGTGCCCAGGSGTGTCTCATCTGGAAGTCTGTGTTTAAACAGACAGTGTG 1062
Db 517 CTGACTACACCGCCCTGTGCCCAGGSGTGTCTCATCTGGAAGTCTGTGTTTAAACAGACAGTGTG 458
Qy 1063 CTGAGTGTAAAGCAGTCCACACCTCTCTGACACCTCTGTGGGAGCTGTGTGACTCTCGG 1122
Db 457 CTGAGTGTAAAGCAGTCCACACCTCTCTGACACCTCTGTGGGAGCTGTGTGACTCTCGG 398
Qy 1123 CTACAGTGTAACTCCGAGCGACGAGCTTGAATGGGCGAGTGTGAGGCTCCCTTC 1182
Db 397 CTACAGTGTAACTCCGAGCGACGAGCTTGAATGGGCGAGTGTGAGGCTCCCTTC 338
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Qy 1243 GTCTGTGTGACATCTCTAGCCCTGTGGTCTCTCTTTTGGCTCTCTTTTGTGTACAGGCTCGG 1302
Db 277 GTCTGTGTGACATCTCTAGCCCTGTGGTCTCTCTTTTGGCTCTCTTTTGTGTACAGGCTCGG 218
Qy 1303 TTCTTTGTGACATGAGAGGAGCAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1362
Db 217 TTCTTTGTGACATGAGAGGAGCAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 158
Qy 1363 CCAGCAGAGGTAGCCGAGACTCGAGC---CTAGAGGCTGGATCTTGGAGAAATGTGAGAAG 1419
Db 157 CCAGCAGAGGTAGCCGAGAACTGGAGCACTAGAGGACATGATCTTGGAGAAATGTGAGAAG 98
Qy 1420 --CCAGCAGAGGATCTGAGGGGAGCCGGTAACTCTCTGTCTCTCTCTCTCTCTCTCTCTCTCT 1476
Db 97 ACACAGCAGAGGATCTGAGGGGAGCCGGTAACTCTCTGTCTCTCTCTCTCTCTCTCTCTCTCTCT 38
Qy 1477 CTTCTTTTAACTGCCAGAAATTTTAAATAAA 1512
Db 37 CTTCTTTTAACTGCCAGAAATTTTAAATAAA 2

RESULT 6
BX401186
LOCUS
DEFINITION
BX401186 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
cDNA clone CS0DK009YP10 5-PRIME, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

REFERENCE 1 (bases 1 to 1201)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5300.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DK009DH05QPl&cluster=5300.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Paraday Avenue Genoscope sequence ID : CS0DK009DH05QPl.
Location/Qualifiers
1..1201
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/clone_line="HELA"
/note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with NotI and cloned into the NotI and EcoRV
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Query Match 54.7%; Score 832; DB 13; Length 1201;
Best Local Similarity 97.4%; Pred. No. 1.2e-174;
Matches 996; Conservative 3; Mismatches 13; Indels 8; Gaps 5;
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DB 110 CTTGCTCAGGCTCACTGTGCAACTGTGCTGCTCACTGCTGCTGCTGCTGCTGCTGCTGCT 169
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QY 181 GATGACCACTGGGCGAGGAGATCTGCCAGTGAAGAGATTCCACCCAGAGAGGAGAT 240
DB 230 GATGACCACTGGGCGAGGAGATCTGCCAGTGAAGAGATTCCACCCAGAGAGGAGAT 289
QY 241 CCACCCGGAGGAGGATCTACTCGAGAGGAGGATCTACCTGGAGAGGAGGATCTACT 300
DB 290 CCACCCGGAGGAGGATCTACTCGAGAGGAGGATCTACTCGAGAGGAGGATCTACT 349
QY 301 GAAGTTAAGCTTAATCAGAGAGAGGAGGCTCCCTGAGCTTAGAGGATCTACTACTGTT 360
DB 350 GAAGTTAAGCTTAATCAGAGAGAGGAGGCTCCCTGAGCTTAGAGGATCTACTACTGTT 409
QY 361 GAGGCTCTGGAGATCTCAAGAACCCAGAAATATGCCCCAGGGAACAGAGGAGAT 420
DB 410 GAGGCTCTGGAGATCTCAAGAACCCAGAAATATGCCCCAGGGAACAGAGGAGAT 469
QY 421 GACCAAGTCAATGGCGCTATGAGGCGACCGCCCTGGCCCGGAGTGTCCCGAGCTGC 480
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QY 481 GCGGGCGGCTTCAGTTCCTGGGTGATATCCGCCCGCCAGCTCGCGGCTTCTGCGCGGCC 540
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QY 841 GCCTTTCTGGAGGAGCGCCCGGAAGAAACAGTGCCTATGAGCAGTTCCTGTCTCGCTTG 900
DB 888 GCCTTTCTGGAGGAGG--CCCGGAAGAAACAGTGCCTATGAGCAGT---TGVTCTCGCT 942
QY 901 GAAGAATCGCTGAGGAGG 920
DB 943 GGWGAATCGCTGAGGAGG 962

RESULT 7
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LOCUS BX423969 Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone
DEFINITION CS0DA003YB12 3-PRIME, mRNA sequence.
ACCESSION BX423969
VERSION BX423969.1 GI:30766327
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1007)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5300.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS1DA0012F09NP1&cluster=5300.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS1DA0012F09NP1.
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
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/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo (dT) primer. Five prime end enriched,
double-strand cDNA was digested with NotI and cloned into
the NotI and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

FEATURES
source
Query Match 53.5%; Score 813.6; DB 13; Length 1007;
Best Local Similarity 89.7%; Pred. No. 1.4e-170;
Matches 852; Conservative 24; Mismatches 71; Indels 3; Gaps 2;

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QY 513 CCCCAGCTCGCGCTTCTGCGCGGCTCGCGCCCTCGAACTCTCTGGGCTTCCAGCT 572
Db 985 CCCCCCGGTCGGCCCTTTTCCCGGCGCGGCGCCCTTGAA--CTCTGGTGTCCGMBT 928
QY 573 CCGCGCGCTCCAGAACTCGCGCTCGCGCAACAATGGCCACAGTGTGCAACTGACCCCTGCC 632
Db 927 CCGCGKGTCCYAGAACTCGG-CTGGGCTAATAGTGCYACAGTGTGCTATYTRACCTCTCC 869
QY 633 TCCTGGGCTAGAGATGGCTCTGGGTCCCGGCGGGAGTACCGGGCTCTGCACTGCAATCT 692
Db 868 TCCTGGGCTATAGATGGTCTGGTTCGCGGCGGGAGTACCGGGCTCTGCGGCTGCTTCT 809
QY 693 GCACTGGGGGCTCGAGTCTCGGCTCGGAGTCCGAGCACACTGTGGAAGGCCACCGTTCCC 752
Db 808 GAATCGGGGTCTCGAGTCTCGGCTCGGAGTCCGAGTCCGAGTCCGAGTCCGAGTCCGAG 749
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QY 873 TGCTATGAGCAGTGTCTGCTGCTTGGAGAAATCGCTGAGGAAGGCTCAGAGACTCA 932
Db 628 TGCTATGAGNAGTGTCTGCTGCTTGGAGAAATCGCTGAGNAGGCTNAGAAACTCA 569
QY 933 GGTCCAGGAGTGCACATATCTGCACTCTCGCTCCCTCTGACTTCAGCGCTACTTCCAATA 992
Db 568 GTTCCAGAGACTGAATNTCTGACNCTGCTCTGACTTCAGCGCGNACTTCCAATT 509
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Db 508 TGAGGGTCTTCTAACTACACCGCGCTGTGCGGCTGTGATCTGACTGTGTTTAAACCA 449
QY 1053 GACAGTATGCTGATGCTGAGAGCTTCCACACCTCTCTGACACCTCTGGGAGCTGG 1112
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QY 1113 TGACTCTCGGCTACAGCTGAATCTCGAGGAGCAGCAGCTTTGAAAGGGGAGTGAATTGA 1172
Db 388 TNACTCTCGGACAGTGTGACTTCCAGGAGCAGCAGCTTTGNAAGGGGAGTGAATTGA 329
QY 1173 GGCTCTCTTCTGCTGAGTGTGAGCAGCTCTCGGGCTGTGAGCAGTCCAGCTGAA 1232
Db 328 GGCTCTCTTCCNGCTGGAGTGAACRAGCTCTCTCGGGCTGTGAGCAGTCCAGCTGAA 269
QY 1233 TTCTGCTGCTGCTGCTGATCTCTAGCCTGCTTTTGGGCTCTCTTTTGGCTGTCTAC 1292
Db 268 TNCCTGCTGCTGCTGCTGATCTCTAGCCTGCTTTTGGGCTCTCTTTTGGCTGTCTAC 209
QY 1293 CAGCGTCCGCTTCTGTCAGATGAGAGGAGCAGCAGAGGAGGAGCAACAAAGGGGTGT 1352
Db 208 CAGCGTCCGCTTCTGTCAGATGAGAGGAGCAGCAGAGGAGGAGCAACAAAGGGGTGT 149
QY 1353 GAGTACCGCCAGCAGAGTGTAGCCAGATCTGAGGCTTGAAGCTGTGATCTTGAAGATG 1412
Db 148 GAGTACCGCCAGCAGAGTGTAGCCAGATCTGAGGCTTGAAGCTGTGATCTTGAAGATG 89
QY 1413 TGAGAGCCAGCCAGAGGCTCTGAGGGGAGGCGGTAACTGCTCTTCC 1462
Db 88 TGAGAGCCAGCCAGAGGCTCTGAGGGGAGGCGGTAACTGCTCTTCC 39

RESULT 8
AL577748/c
LOCUS
DEFINITION
AL577748 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
CDNA clone CS0DK007YK10 3-PRIME, mRNA sequence.
ACCESSION
AL577748
VERSION
AL577748.2 GI:31316001
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KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1031)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 16, 2001 this sequence version replaced gi:12941176.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5300.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DK007BF05NP1&cluster=5300.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ invitrogen Corporation 1600
Paradise Avenue Genoscope sequence ID : CS0DK007BF05NP1.
Location/Qualifiers
FEATURES
source
1..1031
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DK007YK10"
/cell_type="HELA CELLS COT 25-NORMALIZED"
/cell_line="HELA"
/clone_lib="Homo sapiens HELA CELLS COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
Query Match 52.4%; Score 796.8; DB 9; Length 1031;
Best Local Similarity 86.0%; Pred. No. 7.9e-167;
Matches 852; Conservative 50; Mismatches 84; Indels 5; Gaps 4;
QY 521 TCSCCGCTTCTGCGCGGCTCGCGCCCTCGAACTCTCTGGGCTTCCAGCTCCCGCGC 580
Db 989 TCSCCGCGCTTCTGCGCGGCTCGCGCCCTCGAACTCTCTGGGCTTCCAGCTCCCGC 930
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/tissue type="Cell lines"
/dev stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP FL1"
/notes="Organ: Chondrosarcoma; Vector: p773-Pac
(Pharmacia) with a modified polylinker; Site 1: Ecor I;
Site 2: Not I; NCI CGAP FL1 is a normalized cDNA library
derived from a pool of mRNA obtained from 4 cell lines
from grade III chondrosarcoma tissues. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an Ecor I
adaptor, digested with Not I, and cloned directionally
into p773-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
GAGTCCGGTG. The cell lines were provided by Dr. James
Martin from the University of Iowa.
TAG_TISSUE=Human Chondrosarcoma Grade 3 cell line mix
TAG_LIB=UI-H-FL1
TAG_SEQ=GAGTCCGGTG"

ORIGIN

| | | | | |
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| Query Match | 43.4% | Score 560.4 | DB 13 | Length 691 |
| Best Local Similarity | 99.7% | Pred. No. 1.8e-136 | | |
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| Db | 451 | CTCTGACACCCCTGTGGGACCTGGTGACTCTCGGCTACAGCTGAATCTCCGAGCGACGA | 392 | |
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| Db | 391 | GCCTTTGAATGGGCGAGTGATTTGAGGCTCTCCCTGCTGGAGTGACAGCAGTCTCTCG | 332 | |
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| Db | 331 | GGCTGTGAGCCAGTCCAGCTGAATTCCTGCTGGCTGTGCTGACATCTTAGCCCTGGT | 273 | |
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Db 32 TAAATATTATAAT 19
Search completed: May 11, 2004, 16:35:21
Job time : 4193 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 11, 2004, 12:31:03 ; Search time 127 Seconds
(without alignments)

6650.671 Million cell updates/sec

Title: US-09-807-949B-1

Perfect score: 1522

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 2 | 1522 | 100.0 | 1522 | 2 | US-08-477-504A-1 |
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| 5 | 1522 | 100.0 | 1522 | 3 | US-08-787-739-1 |
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ALIGNMENTS

RESULT 1
US-08-481-658B-1
; Sequence 1, Application US/08481658B
; Patent No. 5955075
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 6 Mariposa Court
; CITY: Tiburon
; STATE: California
; COUNTRY: USA
; ZIP: 94920
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,658B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/260,190
; FILING DATE: 15-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-435-2034
; TELEFAX: 415-435-0727
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1522 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEetical: NO
; ANTI-SENSE: NO
US-08-481-658B-1

Query Match 100.0%; Score 1522; DB 2; Length 1522;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
TELEFAX: 415-435-0727
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1522 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-486-756A-1

Query Match 100.0%; Score 1522; DB 2; Length 1522;
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RESULT 4

US-08-485-862B-1
; Sequence 1, Application US/08485862B
; Patent No. 5989838
GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 6 Mariposa Court
; CITY: Tiburon
; STATE: California
; COUNTRY: USA
; ZIP: 94920
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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| 1321 | Db | AGCAGCACAGAAGGGGAAACAAAGGGGGTGTGAGCTACGCCCCAGCAGAGGTAGCCGAG | 1380 |
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| 1381 | Db | ACTGGAGCCTAGAGGCTGGATCTTGGAGAATGTGAGAAGCCAGCCAGAGGCATCTGAGGG | 1440 |
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RESULT 6

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US-08-487-077A-1
; Sequence 1, Application US/08487077A
; Patent No. 6069242
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OP INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; CITY: Tiburon
; STATE: California
; COUNTRY: USA
; ZIP: 94920
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,077A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/260,190
; FILING DATE: 15-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3H
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-435-2034
; TELEFAX: 415-435-0727
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1522 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-487-077A-1

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| Qy | 720 | GGGCGGAGTACCGGGCTCTGCAGCTGCATCTGCATCTGGGGGGCTGCAGTCTGTCCGGC | 720 |
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| Qy | 780 | TCGGAGCACACTGTGGAAGGCCACCGTTTCTGTCCGAGATCCACGTGTGTTCACCTCAGC | 780 |
| Db | 780 | TCGGAGCACACTGTGGAAGGCCACCGTTTCTGTCCGAGATCCACGTGTGTTCACCTCAGC | 780 |
| Qy | 840 | ACCGCTTTGCCAGAGTTGACAGAGCTTGGGGGCGCCGGGAGGCTTGGCCGTGTGGCC | 840 |
| Db | 840 | ACCGCTTTGCCAGAGTTGACAGAGCTTGGGGGCGCCGGGAGGCTTGGCCGTGTGGCC | 840 |
| Qy | 900 | GCCTTTCTGAGGAGGGCCCGGAGAAACAGTGTCTATGAGCAGTGTGTGTCTCGCTTG | 900 |
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| Qy | 960 | GAAGAAATCGCTAGGAAGGCTCAGAGACTCAGGTCCTCCAGGACTGGACATATCTGCACTC | 960 |
| Db | 960 | GAAGAAATCGCTAGGAAGGCTCAGAGACTCAGGTCCTCCAGGACTGGACATATCTGCACTC | 960 |
| Qy | 1020 | CTGCCCTCTCAGTTCAGCCGCTACTTCCAAATATAGGGGTCTCTGTACTACACCGCCCTGT | 1020 |
| Db | 1020 | CTGCCCTCTCAGTTCAGCCGCTACTTCCAAATATAGGGGTCTCTGTACTACACCGCCCTGT | 1020 |
| Qy | 1080 | GCCACGGGTGTCTCTGAGCTGTGTTTAAACAGACAGTGTATGTAGTGTCTTAAGCAGCTC | 1080 |
| Db | 1080 | GCCACGGGTGTCTCTGAGCTGTGTTTAAACAGACAGTGTATGTAGTGTCTTAAGCAGCTC | 1080 |
| Qy | 1140 | CACACCCCTCTGTACACCCCTGTGGGACCTGGTGACTCTCGGCTACAGCTGAACTTCCGA | 1140 |
| Db | 1140 | CACACCCCTCTGTACACCCCTGTGGGACCTGGTGACTCTCGGCTACAGCTGAACTTCCGA | 1140 |

1141 GCGACGAGCCCTTGAATGGGGAGTGATTGAGGCTCCTCCCTGCTGGAGTGACAGC 1200
1141 GCGACGAGCCCTTGAATGGGGAGTGATTGAGGCTCCTCCCTGCTGGAGTGACAGC 1200
1201 AGTCTCGGGCTGTGAGCCAGTCCAGCTGAATTCCTGCTGGCTGCTGCTGACATCCTA 1260
1201 AGTCTCGGGCTGTGAGCCAGTCCAGCTGAATTCCTGCTGGCTGCTGCTGACATCCTA 1260
1261 GCCCTGGTTTGGGCTCCTTTTCTGTCCACAGGCTGCGTTCCTTGTGAGATGAGA 1320
1261 GCCCTGGTTTGGGCTCCTTTTCTGTCCACAGGCTGCGTTCCTTGTGAGATGAGA 1320
1321 AGGACGACAGAAAGGGGACCAAGGGGCTGTGAGTACCGCCAGCAGAGGTAGCCGAG 1380
1321 AGGACGACAGAAAGGGGACCAAGGGGCTGTGAGTACCGCCAGCAGAGGTAGCCGAG 1380
1381 ACTGAGGCTAGAGGCTGGATCTTGGAGAAATGTGAAGCCAGCCAGAGGCATCTGAGGG 1440
1381 ACTGAGGCTAGAGGCTGGATCTTGGAGAAATGTGAAGCCAGCCAGAGGCATCTGAGGG 1440
1441 GGAGCGGTAACTGCTGCTGCTCATATGCCACTTCTTTTAACTGCCAAGAAATT 1500
1441 GGAGCGGTAACTGCTGCTGCTCATATGCCACTTCTTTTAACTGCCAAGAAATT 1500
1501 TTTTAAATAAATAATTATAAT 1522
1501 TTTTAAATAAATAATTATAAT 1522

RESULT 7
US-08-485-863A-1
Sequence 1, Application US/08485863A
Patent No. 603548

GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
CITY: Tiburon
STATE: California
COUNTRY: USA
ZIP: 94920
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,863A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3G
TELEPHONE: 415-435-2034
TELEFAX: 415-435-0727
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1522 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO

ANTI-SENSE: NO
US-08-485-863A-1
Query Match 100.0%; Score 1522; DB 3; Length 1522;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACAGTCAGCCGATGGCTCCCTGTCGCCAGCCCTGGCTCCCTCTGTGTGATCCCGGC 60
DB 1 ACAGTCAGCCGATGGCTCCCTGTCGCCAGCCCTGGCTCCCTCTGTGTGATCCCGGC 60
QY 61 CTTGCTCAGAGCTTCACTGTGCAACTGCTGTGTCTCACTGCTCTTCTGTGATCCCGGC 120
DB 61 CTTGCTCAGAGCTTCACTGTGCAACTGCTGTGTCTCACTGCTCTTCTGTGATCCCGGC 120
QY 121 CCCAGAGGTTGCCCGGATGCGAGAGGATTTCCCTTTGGGAGGAGGCTCTTCTGGGAA 180
DB 121 CCCAGAGGTTGCCCGGATGCGAGAGGATTTCCCTTTGGGAGGAGGCTCTTCTGGGAA 180
QY 181 GATGACCCACTGGGCGAGGAGGATCTGCCAGTGAAGAGGATTCACCCAGAGAGGAGGAT 240
DB 181 GATGACCCACTGGGCGAGGAGGATCTGCCAGTGAAGAGGATTCACCCAGAGAGGAGGAT 240
QY 241 CCACCCGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT 300
DB 241 CCACCCGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT 300
QY 301 GAAATTAAAGCTTAAATCAGAAAGAGGAGGCTCCCTGGAAGTTAGAGGATCTACTACTGT 360
DB 301 GAAATTAAAGCTTAAATCAGAAAGAGGAGGCTCCCTGGAAGTTAGAGGATCTACTACTGT 360
QY 361 GAGGCTCTCTGAGATCTCTCAAGAACCCAGAGATATATGCCACAGGACAAAGAGGAGGAT 420
DB 361 GAGGCTCTCTGAGATCTCTCAAGAACCCAGAGATATATGCCACAGGACAAAGAGGAGGAT 420
QY 421 GACACAGAGTCAATTGGCGCTATGGAGGCGACCCGCTTGGCCCGGGGTGTCCTCAGGCTGC 480
DB 421 GACACAGAGTCAATTGGCGCTATGGAGGCGACCCGCTTGGCCCGGGGTGTCCTCAGGCTGC 480
QY 481 GCGGCGCGTTCAGTCCCGGTGATATCGCCCGGAGCTCGCCGCTTCTGCGCGGC 540
DB 481 GCGGCGCGTTCAGTCCCGGTGATATCGCCCGGAGCTCGCCGCTTCTGCGCGGC 540
QY 541 CTGCGCCCTCTGGAATCTCTGGGCTTCAGAGCTCCCGCGCTCCAGAACTGGCGCTCGC 600
DB 541 CTGCGCCCTCTGGAATCTCTGGGCTTCAGAGCTCCCGCGCTCCAGAACTGGCGCTCGC 600
QY 601 AACAAATGGCCACAGTGTGCAACTGACCTCTCTGGGCTAGAGATGCTCTGGGTCCTC 660
DB 601 AACAAATGGCCACAGTGTGCAACTGACCTCTCTGGGCTAGAGATGCTCTGGGTCCTC 660
QY 661 GGGCGGAGTACCGGCTCTGCACTGCACTGGGGGCTGCAAGTCTGTCGGGC 720
DB 661 GGGCGGAGTACCGGCTCTGCACTGCACTGGGGGCTGCAAGTCTGTCGGGC 720
QY 721 TCGGAGCACACTGTGGAAGGCGCACGTTTCCTGCGGAGATCCACGTGCTTCACTCAGC 780
DB 721 TCGGAGCACACTGTGGAAGGCGCACGTTTCCTGCGGAGATCCACGTGCTTCACTCAGC 780
QY 781 ACCGCTTTTGGCCAGAGTTGACAGAGGCTTGGGCGCCCGGAGGCTGCGCGTGTGGGC 840
DB 781 ACCGCTTTTGGCCAGAGTTGACAGAGGCTTGGGCGCCCGGAGGCTGCGCGTGTGGGC 840
QY 841 GCCTTTCTGGAGAGGCGCCGGAAGAAACAGTGTCTATGAGCAGTGTGCTCTCGCTTG 900
DB 841 GCCTTTCTGGAGAGGCGCCGGAAGAAACAGTGTCTATGAGCAGTGTGCTCTCGCTTG 900
QY 901 GAAGAAATCGCTGAGAGGCTCAGAGACTCAGAGTCCAGAGGCTGACATATCTGCACTC 960
DB 901 GAAGAAATCGCTGAGAGGCTCAGAGACTCAGAGTCCAGAGGCTGACATATCTGCACTC 960
QY 961 CTGCGCTCTGACTTCAAGCGCTTCTTCAATATGAGGGGTCTTGTGACTACCGCCTGT 1020
DB 961 CTGCGCTCTGACTTCAAGCGCTTCTTCAATATGAGGGGTCTTGTGACTACCGCCTGT 1020

421 GACACAGAGTCATTGGCGCTATGGAGCGACCCGCGCTCGCCCGCGGTGTCCCGACCTGC 480
Db
421 GACACAGAGTCATTGGCGCTATGGAGCGACCCGCGCTCGCCCGCGGTGTCCCGACCTGC 480
QY ;
481 GCGGCGCGTTCAGTCCCGGTGTGATATCCGCGCGCGAGCTCGCGCGCTTCTGCGCGGCC 540
Db
481 GCGGCGCGTTCAGTCCCGGTGTGATATCCGCGCGCGAGCTCGCGCGCTTCTGCGCGGCC 540
QY
541 CTGCGCGCGCTCGAGTCTCGGGCTTCAGAGTCCCGCGCTCCAGAACTCGCGCTCGGC 600
Db
541 CTGCGCGCGCTCGAGTCTCGGGCTTCAGAGTCCCGCGCTCCAGAACTCGCGCTCGGC 600
QY
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Db
601 AACAAATGGCCACAGTGTGCAACTGACCTCCCTCTCGGCTAGAGATGCTCTGGGTCCC 660
QY
661 GCGCGGAGTACCGGGCTCTGAGCTGCACTGTGCACTGCGGGGCTGCAAGTGTCTCGGGC 720
Db
661 GCGCGGAGTACCGGGCTCTGAGCTGCACTGTGCACTGCGGGGCTGCAAGTGTCTCGGGC 720
QY
721 TCGGAGCACACTGTGGAAGGCCACCGTTTCCCTGCGGAGATCCAGTGTGTTCACTCAGC 780
Db
721 TCGGAGCACACTGTGGAAGGCCACCGTTTCCCTGCGGAGATCCAGTGTGTTCACTCAGC 780
QY
781 ACCGCGCTTTGCCAGAGTGTGACAGAGCTTTGGGCGCGCCGAGGCTGCGCGTGTGGCC 840
Db
781 ACCGCGCTTTGCCAGAGTGTGACAGAGCTTTGGGCGCGCCGAGGCTGCGCGTGTGGCC 840
QY
841 GCGTTTCTGGAGAGGCGCCGGAAGAAACAGTGTCTATGACAGTGTGCTGTCTGCTTG 900
Db
841 GCGTTTCTGGAGAGGCGCCGGAAGAAACAGTGTCTATGACAGTGTGCTGTCTGCTTG 900
QY
901 GAAGAAATCGCTGAGGAAGGCTCAGAGTCAAGTCCAGGACTGGAATATCTGCATC 960
Db
901 GAAGAAATCGCTGAGGAAGGCTCAGAGTCAAGTCCAGGACTGGAATATCTGCATC 960
QY
961 CTGCGCTCTGACTTCAAGCGGCTTCTTCAATATGAGGGTCTCTGACTACACGCGCTGT 1020
Db
961 CTGCGCTCTGACTTCAAGCGGCTTCTTCAATATGAGGGTCTCTGACTACACGCGCTGT 1020
QY
1021 GCGCAGGCTGATCTGAGTCTGTGTTTAAACAGACAGTGTGCTGAGTGTCTGAGCAGTCT 1080
Db
1021 GCGCAGGCTGATCTGAGTCTGTGTTTAAACAGACAGTGTGCTGAGTGTCTGAGCAGTCT 1080
QY
1081 CACACCTCTCTGACACCTGTGGGACCTGTGACTCTCGGCTACAGTGAATCTCGA 1140
Db
1081 CACACCTCTCTGACACCTGTGGGACCTGTGACTCTCGGCTACAGTGAATCTCGA 1140
QY
1141 GCGAGCAGCCTTTGAATGGGCGAGTGAATGAGGCTCTCTTCCCTGCTGGAGTGACAGC 1200
Db
1141 GCGAGCAGCCTTTGAATGGGCGAGTGAATGAGGCTCTCTTCCCTGCTGGAGTGACAGC 1200
QY
1201 AGTCTCGGGCTGTGAGCAGTCCAGTGAATTCCTGCTGGCTGTGCTGAGTGAATCTTA 1260
Db
1201 AGTCTCGGGCTGTGAGCAGTCCAGTGAATTCCTGCTGGCTGTGCTGAGTGAATCTTA 1260
QY
1261 GCGCTGTTTTGGCTCTCTTTTGTGTGTCACAGCGTGTGCTGCTGCTGAGTGAATGAG 1320
Db
1261 GCGCTGTTTTGGCTCTCTTTTGTGTGTCACAGCGTGTGCTGCTGAGTGAATGAG 1320
QY
1321 AGGAGCAGCAGAGAGGGAACCAAGGGGTGTGAGTACCGGCCAGCAGAGGTAGCCGAG 1380
Db
1321 AGGAGCAGCAGAGAGGGAACCAAGGGGTGTGAGTACCGGCCAGCAGAGGTAGCCGAG 1380
QY
1381 ACTGAGGCTTAGAGGCTGATCTTGAGAAATGTGAGAACCGCAGAGGCTCTGAGGG 1440
Db
1381 ACTGAGGCTTAGAGGCTGATCTTGAGAAATGTGAGAACCGCAGAGGCTCTGAGGG 1440
QY
1441 GAGAGCGGTAACTGCTCTGCTGCTCATTTATGCTCACTTTTAACTGCCAAGAAAT 1500
Db
1441 GAGAGCGGTAACTGCTCTGCTGCTCATTTATGCTCACTTTTAACTGCCAAGAAAT 1500
QY
1501 TTTTAAAAATAAATATTATAAT 1522

Db 1501 TTTTAAAAATAAATATTATAAT 1522
RESULT 11
US-08-335-469-1
; Sequence 1, Application US/08335469A
; Patent No. 6004535
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: Methods to Detect and Quantify MN Protein/Polypeptide
; FILE REFERENCE: D-0021A
; CURRENT APPLICATION NUMBER: US/08/335,469A
; CURRENT FILING DATE: 1994-11-07
; EARLIER APPLICATION NUMBER: 07/964,589
; EARLIER FILING DATE: 1992-10-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1399
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1266)
US-08-335-469-1
Query Match 91.9%; Score 1399; DB 3; Length 1399;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1399; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 124 CAGAGTTGCCCCCGATGTCAGAGGATTTCCCTTGGAGAGGCTCTCTGGGAAGAT 183
Db 1 CAGAGTTGCCCCCGATGTCAGAGGATTTCCCTTGGAGAGGCTCTCTGGGAAGAT 60
QY 184 GACCCACTGGCGGAGGAGGATCTGCCAGTGAAGAGGATTCACCCAGAGAGGAGATCCA 243
Db 61 GACCCACTGGCGGAGGAGGATCTGCCAGTGAAGAGGATTCACCCAGAGAGGAGATCCA 120
QY 244 CCGGAGAGGAGGATCTACTGGAGAGGAGATCTACTGGAGAGGAGATCTACTGAA 303
Db 121 CCGGAGAGGAGGATCTACTGGAGAGGAGATCTACTGGAGAGGAGATCTACTGAA 180
QY 304 GTTAAGCCTTAATCAGAGAGAGGCTCCCTGAAGTTAGAGGATCTACTGTTGAG 363
Db 181 GTTAAGCCTTAATCAGAGAGAGGCTCCCTGAAGTTAGAGGATCTACTGTTGAG 240
QY 364 GCTCTGAGAGATCTCAAGAACCCAGAGATTAATGCCACAGGACAAAGAGGGAGTAC 423
Db 241 GCTCTGAGAGATCTCAAGAACCCAGAGATTAATGCCACAGGACAAAGAGGGAGTAC 300
QY 424 CAGAGTCAATTGGCGCTATGAGAGGAGACCCGCTTGGCGCCCGGGTGTCCCAGCCTGCGG 483
Db 301 CAGAGTCAATTGGCGCTATGAGAGGAGACCCGCTTGGCGCCCGGGTGTCCCAGCCTGCGG 360
QY 484 GCGCGCTTCCAGTCCCGGTGATATCGCGCCCGAGCTCGCGCCCTCTGCGCGGCCCTG 543
Db 361 GCGCGCTTCCAGTCCCGGTGATATCGCGCCCGAGCTCGCGCCCTCTGCGCGGCCCTG 420
QY 544 GCGCGCTTCCAGTCCCGGTGATATCGCGCCCGAGCTCGCGCCCTCTGCGCGGCCCTG 603
Db 421 GCGCGCTTCCAGTCCCGGTGATATCGCGCCCGAGCTCGCGCCCTCTGCGCGGCCCTG 480
QY 604 AATGCCCAAGTGTGCAACTGACCTGCTCTGCGGCTAGAGATGCTCTGGGTCCCGGG 663
Db 481 AATGCCCAAGTGTGCAACTGACCTGCTCTGCGGCTAGAGATGCTCTGGGTCCCGGG 540
QY 664 CCGGAGTACCGGCTCTGAGCTGATCTGCACTGGGGGCTGCAAGTCTCGGGGCTG 723
Db 541 CCGGAGTACCGGCTCTGAGCTGATCTGCACTGGGGGCTGCAAGTCTCGGGGCTG 600

663 GCGGAGTACCGGGCTCTGACGTGCTGACCTGGGGGGCTGACGGTCTGCGGGCTC 722
DB |||||
538 GCGGAGTACC-GGCTCTGACGTGCTGACCTGGGGGGCTGACGGTCTGCGGGCTC 596
QY |||||
723 GGAGCACTGTGGAAGCCACGGTTTCCCTCCGAGATCCACGTGGTTTCACTCAGCAC 782
DB |||||
597 GGAGCACACTGTGGAAGCCACGGTTTCCCTCCGAGATCCACGTGGTTTCACTCAGCAC 656
QY |||||
783 CGCCTTTCAGAGTGTGACGAGCCCTTGGGGGGCCCGGGAGGCTGGCGGTGGCGCCG 842
DB |||||
657 CGCCTTTCAGAGTGTGACGAGCCCTTGGGGGGCCCGGGAGGCTGGCGGTGGCG-CGC 715
QY |||||
843 CTTTCTGGAGAGGGGCCCGAAGAAACAGTG-CCTATGAGCAGTTTGTCTCTCGCTGG 901
DB |||||
716 CTTTCTGGAGAGGGGCCCGAAGAAACAGTGCTCTATGAGCAGTTTGTCTCTCGCTGG 775
QY |||||
902 AAGAAATCCTGAGGAAGGCTCAGAGACTCAGGTGCCAGGATGAGACATATCTGCACTCC 961
DB |||||
776 AAGAAATCCTGAGGAAGGCTCAGAGACTCAGGTGCCAGGATGAGACATATCTGCACTCC 835
QY |||||
962 TGCCTCTGACTTCAAGCCCTACTTCCAAATATGAGGGTCTCTGACTACACCGCCCTGG 1021
DB |||||
836 TGCCTCTGACTTCAAGCCCTACTTCCAAATATGAGGGTCTCTGACTACACCGCCCTGG 895
QY |||||
1022 CCCAGGCTCTGACTTCAAGCCCTACTTCCAAATATGAGGGTCTCTGACTACACCGCTCC 1081
DB |||||
896 CCCAGGCTCTGACTTCAAGCCCTACTTCCAAATATGAGGGTCTCTGACTACACCGCTCC 955
QY |||||
1082 ACACCCCTCTGACACCCCTGTGGGACCTGGTGAATCTCGGCTACAGCTGAATCTCCGAG 1141
DB |||||
956 ACACCCCTCTGACACCCCTGTGGGACCTGGTGAATCTCGGCTACAGCTGAATCTCCGAG 1015
QY |||||
1142 CACGCGAGCTTGAATGGGCGAGTGAATGAGCCCTCTTCCCTGCTGGAGTGACGCA 1201
DB |||||
1016 CAGCGAGCTTGAATGGGCGAGTGAATGAGCCCTCTTCCCTGCTGGAGTGACGCA 1075
QY |||||
1202 GTCTCTGGGCTGCTGAGCGAGTCCAGCTGAATCTCTGCTGCTGCTGCTGCTGCTGCTAG 1261
DB |||||
1076 GTCTCTGGGCTGCTGAGCGAGTCCAGCTGAATCTCTGCTGCTGCTGCTGCTGCTGCTAG 1135
QY |||||
1262 CCCTGTTTTTGGCTCTCTTTTGTGCTGCTCAAGCGTTCGGTTCCTTGTGACGATGAGAA 1321
DB |||||
1136 CCCTGTTTTTGGCTCTCTTTTGTGCTGCTCAAGCGTTCGGTTCCTTGTGACGATGAGAA 1195
QY |||||
1322 GGCACACAGAGGGGAAACCAAGGGGTGTGAGC-TACGCGCCAGCAGAGGTAGCGAG 1380
DB |||||
1196 GGCACACAGAGGGGAAACCAAGGGGTGTGAGCGTACCGCCAGCAGAGGTAGCGAG 1255
QY |||||
1381 ACTGGAGCCTAGAGGCTGGATCTTGGAGAAATGTGAGAACCCAGCCAGAGGCTCTGAGGG 1440
DB |||||
1256 ACTGGAGCCTAGAGGCTGGATCTTGGAGAAATGTGAGAACCCAGCCAGAGGCTCTGAGGG 1315
QY |||||
1441 GGAGCGGTAACTGCTCTCTGCTCATTTATGCACTTCTTTTAACTGCCAAGAAATT 1500
DB |||||
1316 GGAGCGGTAACTGCTCTCTGCTCATTTATGCACTTCTTTTAACTGCCAAGAAATT 1375
QY |||||
1501 TTTTAAATTAATTTATAAT 1522
DB |||||
1376 TTTTAAATTAATTTATAAT 1397

RESULT 13
PCT-US93-02024-1
; Sequence 1, Application PC/TUS9302024
; GENERAL INFORMATION:
; APPLICANT: CIBA Corning Diagnostics Corp.
; APPLICANT: Institute of Virology
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: Stuart Street Tower, 18th Fl., One Market
; STREET: Plaza

CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/02024
FILING DATE: 19930308
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CS PV-709-92
FILING DATE: 10-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/964,589
FILING DATE: 21-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-777-9257
TELEFAX: 415-543-4219
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1397 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1287
PCT-US93-02024-1

Query Match 85.6%; Score 1302.8; DB 5; Length 1397;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 1392; Conservative 0; Mismatches 2; Indels 8; Gaps 8;
QY 124 CAGAGGTTGCCCCCGATCCAGGAGGATTCCTCCCTTGGAGGAGGCTCTTCTCGGGAAGAT 183
DB 1 CAGAGGTTGCCCCCGATCCAGGAGGATTCCTCCCTTGGAGGAGGCTCTTCTCGGGAAGAT 59
QY 184 GACCCACTGGGCGAGGAGGATCTGCCAGTGAAGAGGATTCACCCAGAGAGGAGGATCCA 243
DB 60 GACCCACTGGGCGAGGAGGATCTGCCAGTGAAGAGGATTCACCCAGAGAGGAGGATCCA 119
QY 244 CCCGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGAA 303
DB 120 CCCGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGAA 179
QY 304 GTTAA-GCCTAAATCAGAGAGGAGGCTCCTCTGAAGTTAGAGGATCTACCTACTGTTCA 362
DB 180 GTTAAATGCTTAAATCAGAGAGGAGGCTCCTCTGAAGTTAGAGGATCTACCTACTGTTCA 239
QY 363 GGCTCTCGAGATCTCTCAAGAACCCAGAAATATCCCAAGAGGACAAAGAGGGGATGA 422
DB 240 GGCTCTCGAGATCTCTCAAGAACCCAGAAATATCCCAAGAGGACAAAGAGGGGATGA 299
QY 423 CCAGAGTCAATTGGCGCTATGAGAGGAGACCCGCGCTGGCGCCCGGGGTGTCCTCCAGCTGCGC 482
DB 300 CCAGAGTCAATTGGCGCTATGAGAGGAGACCCG-CCTGGCGCCCGGGGTGTCCTCCAGCTGCGC 358
QY 483 GGGCGCTTTCAGTCCCGGCTGATATCGCCCGCCAGCTCGCGGCTCTCTCGCCGCGCT 542
DB 359 GGGCGCTTTCAGTCCCGGCTGATATCGCCCGCCAGCTCGCGGCTCTCTCGCCGCGCT 418
QY 543 GGGCGCTTTCAGTCTCTCGGCTCTCCAGCTCGCGGCTCTCCAGAACTCGCGCTCGCA 602

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|------|----|--|-----|----|-----|-----|-----|-----|-----|-----|----|----|-----|----|-----|-----|-----|-----|----|-----|-----|-----|-----|-----|----|-----|----|-----|-----|-----|------|------|
| 419 | Db | | GC | CC | CC | CT | GG | AA | CT | CT | TG | GG | CT | TC | CAG | CT | CC | CG | CG | CT | CC | CAG | AA | TG | CG | CT | GC | - | AGA | 477 | | |
| 603 | Qy | | CAA | TG | GC | CA | CAG | TG | TG | CA | CT | GA | CC | CT | GC | CT | TG | GG | CT | TAG | AG | AT | GG | CT | CT | GG | CT | CC | CG | 662 | | |
| 478 | Db | | CAA | TG | GC | CA | CAG | TG | TG | CA | CT | GA | CC | CT | GC | CT | TG | GG | CT | TAG | AG | AT | GG | CT | CT | GG | CT | CC | CG | 537 | | |
| 663 | Qy | | GC | GG | AG | TAC | CG | GG | CT | TC | GA | GT | CA | CT | TC | GA | CT | TG | GG | GG | GG | CT | TC | GA | GT | CT | CG | GG | CT | 722 | | |
| 538 | Db | | GC | GG | AG | TAC | - | GG | CT | TC | GA | GT | CA | CT | TC | GA | CT | TG | GG | GG | GG | CT | TC | GA | GT | CT | CG | GG | CT | 596 | | |
| 723 | Qy | | GG | AG | CAC | AT | GT | GG | AA | GG | CC | AC | CG | TT | TCC | CT | CG | CG | AG | AT | CC | AG | TG | GT | T | CAC | CT | CAG | CAC | 782 | | |
| 597 | Db | | GG | AG | CAC | AT | GT | GG | AA | GG | CC | AC | CG | TT | TCC | CT | CG | CG | AG | AT | CC | AG | TG | GT | T | CAC | CT | CAG | CAC | 656 | | |
| 783 | Qy | | CG | CC | TT | GC | CAG | AT | TGA | CG | AG | GC | TT | TG | GG | GG | CG | CG | CG | GG | AG | GC | CT | GG | CG | TG | TG | GG | CG | 842 | | |
| 657 | Db | | CG | CC | TT | TG | CAG | AT | TGA | CG | AG | GC | TT | TG | GG | GG | CG | CG | CG | GG | AG | GC | CT | GG | CG | TG | TG | TG | - | CG | 715 | |
| 843 | Qy | | CT | TT | CT | TG | GG | AG | GG | CC | CG | GA | AA | CA | CG | TG | - | CT | AT | GA | GC | AG | TG | TC | GT | CT | CG | CT | TG | 901 | | |
| 716 | Db | | CT | TT | CT | TG | GG | AG | GG | CC | CG | GA | AA | CA | CG | TG | TC | AT | GA | GC | AG | TG | TC | GT | CT | CG | CT | TG | CT | 775 | | |
| 902 | Qy | | AA | GA | AT | CG | CT | GAG | GA | GG | CT | CA | GAG | CT | CAG | GT | CC | AG | GA | CT | GG | CA | TAT | TC | GC | ACT | TC | | | 961 | | |
| 776 | Db | | AA | GA | AT | CG | CT | GAG | GA | GG | CT | CA | GAG | CT | CAG | GT | CC | AG | GA | CT | GG | CA | TAT | TC | GC | ACT | TC | | | 835 | | |
| 962 | Qy | | TG | CC | CT | TC | GA | CT | T | CAG | CC | GC | TA | CT | T | CCA | TAT | GA | GG | GT | CT | TC | GA | CT | T | CA | CC | CC | CT | TG | 1021 | |
| 836 | Db | | TG | CC | CT | TC | GA | CT | T | CAG | CC | GC | TA | CT | T | CCA | TAT | GA | GG | GT | CT | TC | GA | CT | T | CA | CC | CC | CT | TG | 895 | |
| 1022 | Qy | | CC | CA | GG | GT | GC | AT | CT | GG | AC | TG | TT | T | AA | CC | AG | CA | GC | AT | GA | TG | CT | GC | AG | TG | CT | TA | AG | CAG | CT | 1081 |
| 896 | Db | | CC | CA | GG | GT | GC | AT | CT | GG | AC | TG | TT | T | AA | CC | AG | CA | GC | AT | GA | TG | CT | GC | AG | TG | CT | TA | AG | CAG | CT | 955 |
| 1082 | Qy | | ACA | CC | CT | CT | CA | CA | CC | CT | TG | GG | GA | CT | GG | TA | CT | CG | GG | CT | TAC | AG | CT | GAA | CT | T | CC | GA | | | 1141 | |
| 956 | Db | | ACA | CC | CT | CT | CA | CA | CC | CT | TG | GG | GA | CT | GG | TA | CT | CG | GG | CT | TAC | AG | CT | GAA | CT | T | CC | GA | | | 1015 | |
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APPLICANT: Zavada, Jan
 APPLICANT: Pastorekova, Silvia
 APPLICANT: Pastorek, Jaromir
 TITLE OF INVENTION: MN Gene and Protein
 NUMBER OF SEQUENCES: 86
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Leona L. Lauder
 STREET: 6 Mariposa Court
 CITY: Tiburon
 STATE: California
 COUNTRY: USA
 ZIP: 94920
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/481,658B
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/260,190
 FILING DATE: 15-JUN-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Lauder, Leona L.
 REGISTRATION NUMBER: 30,863
 REFERENCE/DOCKET NUMBER: D-0021.3E
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-435-2034
 TELEFAX: 415-435-0727
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10898 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 US-08-481-658B-5

| Query Match | 27.2%; | Score 414.4; | DB 2; | Length 10898; |
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| Best Local Similarity | 99.8%; | Pred. No. 7.4e-94; | | |
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| QY | 61 | CTGTCTCCAGGCTCACTGTGCAACTGTCTGTCTACTGTCTGTCTGTGATGCTGTCCAT | 120 | |
| DB | 3597 | CTGTCTCCAGGCTCACTGTGCAACTGTCTGTCTACTGTCTGTCTGTGATGCTGTCCAT | 3656 | |
| QY | 121 | CCCCAGAGTTGCCCGGATGACGAGGAGTCCCCCTTGGGAGGAGCTCTTCTGGGAA | 180 | |
| DB | 3657 | CCCCAGAGTTGCCCGGATGACGAGGAGTCCCCCTTGGGAGGAGCTCTTCTGGGAA | 3716 | |
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| DB | 3717 | GATGACCCACTGGGCGAGGAGGATCTGCCAGTGAAGAGGATTCACCCAGAGAGGAGGAT | 3776 | |
| QY | 241 | CCACCCGGAGAGGAGATCTTACTTGAGAGGAGGATCTTACTTGAGAGGAGGATCTACCT | 300 | |
| DB | 3777 | CCACCCGGAGAGGAGATCTTACTTGAGAGGAGGATCTTACTTGAGAGGAGGATCTACCT | 3836 | |
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OM nucleic - nucleic search, using sw model

Run on: May 11, 2004, 13:34:08 ; Search time 694 Seconds
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Searched: 2941586 seqs, 2264995651 residues

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 2 | 1522 | 100.0 | 1522 | 10 | US-09-967-237-1 |
| 3 | 1522 | 100.0 | 1522 | 9 | US-09-954-456-89 |
| 4 | 1522 | 100.0 | 1522 | 9 | US-09-954-456-726 |
| 5 | 1522 | 100.0 | 1522 | 10 | US-09-960-706-1080 |
| 6 | 1522 | 100.0 | 1522 | 10 | US-09-873-367C-516 |
| 7 | 1522 | 100.0 | 1522 | 13 | US-10-342-887-574 |
| 8 | 1522 | 100.0 | 1522 | 13 | US-10-172-118-574 |
| 9 | 1522 | 100.0 | 1522 | 13 | US-10-388-360-291 |
| 10 | 1522 | 100.0 | 1522 | 15 | US-10-301-822-11 |
| 11 | 1522 | 100.0 | 1522 | 16 | US-10-465-572-9 |
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Sequence 35, Appli

ALIGNMENTS

RESULT 1

US-09-772-719-1
; Sequence 1, Application US/09772719
; Patent No. US20020137910A1
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 369 Pine Street
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/772,719
; FILING DATE: 30-JAN-2001
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,049
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/260,190
; FILING DATE: 15-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-981-2034

TELEFAX: 415-981-0332
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 1322 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-772-719-1

| Query Match | 100.0% | Score 1522; | DB 9; | Length 1522; |
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| Best Local Similarity | 100.0%; | Pred. No. 0; | | |
| Matches 1522; | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0 |
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| Db | 1 | ACAGTCAGCGCATGGCTCCCTCTGCCCCAGCCCTGCGCTCCCTCTGTGATCCCGGCC | 60 | |
| Qy | 61 | CTTGCTCCAGGCTCACTGTGCAACTGTCTGTCTGCTCACTGCTGCTTCTGATGCTGTCCAT | 120 | |
| Db | 61 | CTTGCTCCAGGCTCACTGTGCAACTGTCTGTCTGCTCACTGCTGCTTCTGATGCTGTCCAT | 120 | |
| Qy | 121 | CCCCAGAGTTGCCCGGATCGAGAGATTCCCTCTGGAGAGAGGCTCTTCTGGGGAA | 180 | |
| Db | 121 | CCCCAGAGTTGCCCGGATCGAGAGATTCCCTCTGGAGAGAGGCTCTTCTGGGGAA | 180 | |
| Qy | 181 | GATGACCCACTGGCGGAGGAGTCTGCCCACTGAGAGGATTACCCAGAGAGGAGAT | 240 | |
| Db | 181 | GATGACCCACTGGCGGAGGAGTCTGCCCACTGAGAGGATTACCCAGAGAGGAGAT | 240 | |
| Qy | 241 | CCACCCGAGAGGAGGATCTACTTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACT | 300 | |
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| Qy | 301 | GAAGTTAAGCCTAAATCAGAGAAGAGGGCTCCCTGAAAGTTAGAGGATCTACTACTGTT | 360 | |
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| Qy | 361 | GAGGCTCTTGAGATCTCTAAGAACCCAGAAATAATGCCACAGGGAACAAGAGGGGAT | 420 | |
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| Qy | 421 | GACCAGAGTCAATTGCGGTATGAGGCGACCCGCGCTGGCGCCCGGGTGTCCCCAGCCTGC | 480 | |
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| Qy | 481 | CGCGGCGCTTCCAGTCCCGGTGGATATCCGCCCCCAGCTGCGCGCTTCTGCGCCGCGC | 540 | |
| Db | 481 | CGCGGCGCTTCCAGTCCCGGTGGATATCCGCCCCCAGCTGCGCGCTTCTGCGCCGCGC | 540 | |
| Qy | 541 | CTGCGGCGCTTGGAACTCTCTGGGCTTCCAGTCTCCGCGCGCTCCAGAACTGGCGCTGGC | 600 | |
| Db | 541 | CTGCGGCGCTTGGAACTCTCTGGGCTTCCAGTCTCCGCGCGCTCCAGAACTGGCGCTGGC | 600 | |
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| Db | 601 | AACAAATGSCCACTGTGCAACTGACCTGCTCTGGCTAGAGATGCTCTGGGTCCC | 660 | |
| Qy | 661 | GGCGGGAGTACCGGGCTCTGAGCTGATCTGCACTGGGGGGCTGAGTCTGTCGGGCG | 720 | |
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| Db | 781 | ACCGCTTTGCCAGAGTTGACAGGCTTTGGGGCGCCGCGGAGGCTCTGCGCTGTTGCC | 840 | |
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RESULT 2
US-09-967-237-1
; Sequence 1, Application US/09967237
; Publication No. US20030049828A1
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; FILE REFERENCE: D-0021.5B-2
; CURRENT APPLICATION NUMBER: US/09/967,237
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 09/178,115
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1522
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (13)..(1389)
; NAME/KEY: mat_peptide
; LOCATION: (124)..(1389)

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751 TCGGAGCACACTGTGGAAGGCGACCTGCTCCCTGCGAGATCCACGTGTTTCACTCAGC 810
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RESULT 7

US-10-342-887-574
; Sequence 574, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10/342,887
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2659
; SEQ ID NO 574
; LENGTH: 1552
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-342-887-574

Query Match 100.0%; Score 1522; DB 13; Length 1552;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 661 GCGCGGAGTACCGGCTCTGAGCTGCACTGCACTGGGGGGCTGCAAGTCTGCGGGC 720
Db 691 GCGCGGAGTACCGGCTCTGAGCTGCACTGCACTGGGGGGCTGCAAGTCTGCGGGC 750
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Db 751 TCGGAGCACTGTGGAAGGCCACCGTTCCCTGCCGAGATCCAGTGTTCACCTCAGC 810
Qy 781 ACCGCTTTGCCAGAGTTCACAGAGGCTTGGGGCGCCCGGAGGCTGCGCTGTGGCC 840
Db 811 ACCGCTTTGCCAGAGTTCACAGAGGCTTGGGGCGCCCGGAGGCTGCGCTGTGGCC 870
Qy 841 GCCTTTCTGGAGAGGCGCCGGAAGAAAACAGTGCCTATGAGCAGTGTCTGCTGCTTG 900
Db 871 GCCTTTCTGGAGAGGCGCCGGAAGAAAACAGTGCCTATGAGCAGTGTCTGCTGCTTG 930
Qy 901 GAAGAAATCGTGAGAAAGGCTCAGACACTCAGGTCCCGAGGACTGACATATCTGCACTC 960
Db 931 GAAGAAATCGTGAGAAAGGCTCAGACACTCAGGTCCCGAGGACTGACATATCTGCACTC 990
Qy 961 CTGCCCTCTGACTTCAGCGCTACTTCCAAATATGAGGGTCTCTGACTACACCGCCCTGT 1020
Db 991 CTGCCCTCTGACTTCAGCGCTACTTCCAAATATGAGGGTCTCTGACTACACCGCCCTGT 1050
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Db 1111 CACACCTCTCTGACACCTGTGGGACCTGTGACTCTCGGCTACAGCTGAATTTCCGA 1170
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Qy 1201 AGTCTCTGGGCTCTGAGCCAGTCCAGCTGAATTTCTTCCCTGCTGCTGCTGCTGCTGCT 1260
Db 1231 AGTCTCTGGGCTCTGAGCCAGTCCAGCTGAATTTCTTCCCTGCTGCTGCTGCTGCTGCT 1290
Qy 1261 GCCTGGTTTTGGCTCTCTTTTGTGTGTCACAGAGGTGCGGTTCTTGTGCGAGATGAGA 1320
Db 1291 GCCTGGTTTTGGCTCTCTTTTGTGTGTCACAGAGGTGCGGTTCTTGTGCGAGATGAGA 1350

RESULT 8

US-10-172-118-574
; Sequence 574, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 574
; LENGTH: 1552
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM_001216
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-574

Query Match 100.0%; Score 1522; DB 13; Length 1552;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACAGTCAGCGCGCATGGCTCCCTGTCGCCAGCCCTGGCTCCCTCTCTGTTGATCCCGGCC 60
Db 31 ACAGTCAGCGCGCATGGCTCCCTGTCGCCAGCCCTGGCTCCCTCTCTGTTGATCCCGGCC 90
Qy 61 CTGCTCCAGGCTCACTGTGCAACTGTGTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 120
Db 91 CTGCTCCAGGCTCACTGTGCAACTGTGTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 150
Qy 121 CCCGAGAGTTCCCGGATGCGAGGATTTCCCTTTGGGAGGAGGCTCTTCTGGGGAA 180
Db 151 CCCGAGAGTTCCCGGATGCGAGGATTTCCCTTTGGGAGGAGGCTCTTCTGGGGAA 210
Qy 181 GATGACCCACTGGCGAGGAGGATCTGCCAGTGAAGAGGATTCACCCAGAGAGGAGGAT 240
Db 211 GATGACCCACTGGCGAGGAGGATCTGCCAGTGAAGAGGATTCACCCAGAGAGGAGGAT 270
Qy 241 CCACCCGGAGAGGAGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT 300
Db 271 CCACCCGGAGAGGAGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT 330
Qy 301 GAAGTTAAGCCCTAAATCAGAAAGAGGCTCCCTGAAAGTTAGAGGATCTACCTACTGTT 360

| | | | | |
|----|--|------|---|------|
| Qy | | 481 | GCGGGCGCCTTCAGATCCCCGGTGGGAATCCGCCGCCAGCTCGCCGCTCTTGCCCGGCC | 540 |
| Db | | 511 | GCGGGCGCCTTCAGATCCCCGGTGGGAATCCGCCGCCAGCTCGCCGCTCTTGCCCGGCC | 570 |
| Qy | | 541 | CTGGGCCCCCTGGAACCTCTGGGCTTCCAGCTCCCGCCGTCCAGAACTGGCCCTTCGC | 600 |
| Db | | 571 | CTGGGCCCCCTGGAACCTCTGGGCTTCCAGCTCCCGCCGTCCAGAACTGGCCCTTCGC | 630 |
| Qy | | 601 | AACAATGGCCCAAGTGTGCAACTGACCCTGCCTCTGGGTAGAGATGGCTTGGGTCCC | 660 |
| Db | | 631 | AACAATGGCCCAAGTGTGCAACTGACCCTGCCTCTGGGTAGAGATGGCTTGGGTCCC | 690 |
| Qy | | 661 | GGGGGAGTACCGGGCTCTGCAGCTGCATCTGCACTGGGGGGCTCGAGTCTGCGGGC | 720 |
| Db | | 691 | GGGGGAGTACCGGGCTCTGCAGCTGCATCTGCACTGGGGGGCTCGAGTCTGCGGGC | 750 |
| Qy | | 721 | TGGAGACACACTGTGGAAGGCCACCGCTTTCCCTGCCGAGATCCAAGTGTTCACCTCAGC | 780 |
| Db | | 751 | TGGAGACACACTGTGGAAGGCCACCGCTTTCCCTGCCGAGATCCAAGTGTTCACCTCAGC | 810 |
| Qy | | 781 | ACGCCCTTTGCGAGAGTTGAGAGGCCCTTGGGGGCCCGGGAGGCCCTGGCCGTGTGGCC | 840 |
| Db | | 811 | ACGCCCTTTGCGAGAGTTGAGAGGCCCTTGGGGGCCCGGGAGGCCCTGGCCGTGTGGCC | 870 |
| Qy | | 841 | GCCCTTCTGGAGGAGGCCCGGAAGAAAAAGTGCCTATCAGCAGATTGCTGTCTCGCTTG | 900 |
| Db | | 871 | GCCCTTCTGGAGGAGGCCCGGAAGAAAAAGTGCCTATCAGCAGATTGCTGTCTCGCTTG | 930 |
| Qy | | 901 | GAAGAAATCGCTGAGGAGGCTCAGAGACTCAGGTCCCAGGATGGAACATATCTGCATC | 960 |
| Db | | 931 | GAAGAAATCGCTGAGGAGGCTCAGAGACTCAGGTCCCAGGATGGAACATATCTGCATC | 990 |
| Qy | | 961 | CTGCCCTCTGACTTCAGCGCTACTTCCAAATATGAGGGGTCTCTGACTACACCGCCCTGT | 1020 |
| Db | | 991 | CTGCCCTCTGACTTCAGCGCTACTTCCAAATATGAGGGGTCTCTGACTACACCGCCCTGT | 1050 |
| Qy | | 1021 | GCCCAGGGTGTCACTCGEACTGTGTTTAACAGACAGTGAATGCTGAGTGTAAAGCAGCTC | 1080 |
| Db | | 1051 | GCCCAGGGTGTCACTCGEACTGTGTTTAACAGACAGTGAATGCTGAGTGTAAAGCAGCTC | 1110 |
| Qy | | 1081 | CACACCTCTCTGACACCTGTGGGACCTGTGTGATCTCTGGCTACAGCTGAATCTCCGA | 1140 |
| Db | | 1111 | CACACCTCTCTGACACCTGTGGGACCTGTGTGATCTCTGGCTACAGCTGAATCTCCGA | 1170 |
| Qy | | 1141 | CGACGACAGCTTTGAATGGGCGAGTGAATTGAGGCCCTCTTCCCTGCTGAGTGGACAGC | 1200 |
| Db | | 1171 | CGACGACAGCTTTGAATGGGCGAGTGAATTGAGGCCCTCTTCCCTGCTGAGTGGACAGC | 1230 |
| Qy | | 1201 | AGTCTCTCGGGCTGTGAGCCAGTCCAGCTGAAATTCCTGCTGGCTGTGTGTGATCATCTTA | 1260 |
| Db | | 1231 | AGTCTCTCGGGCTGTGAGCCAGTCCAGCTGAAATTCCTGCTGGCTGTGTGTGATCATCTTA | 1290 |
| Qy | | 1261 | GCCCTGTTTTTGGCTCTCTTTTGTGCTCACAGCGTCCGGTCTCTTGTGTCAGATGAGA | 1320 |
| Db | | 1291 | GCCCTGTTTTTGGCTCTCTTTTGTGCTCACAGCGTCCGGTCTCTTGTGTCAGATGAGA | 1350 |
| Qy | | 1321 | AGGCAGCAGAGAGGGGAAACAAAGGGGGTGTGAGCTACCGCCAGCAGAGGTAGCCGAG | 1380 |
| Db | | 1351 | AGGCAGCAGAGAGGGGAAACAAAGGGGGTGTGAGCTACCGCCAGCAGAGGTAGCCGAG | 1410 |
| Qy | | 1381 | ACTGGAGCTTAGAGCTTGATCTTTGGAGAATGTGAGAGCCAGCCAGAGGCATCTGAGGG | 1440 |
| Db | | 1411 | ACTGGAGCTTAGAGCTTGATCTTTGGAGAATGTGAGAGCCAGCCAGAGGCATCTGAGGG | 1470 |
| Qy | | 1441 | GGAGCGGTAACTCTCTGTCTCTCTCATATATGCCACTTCTTTTAACCTCCCAAGAAATT | 1500 |
| Db | | 1471 | GGAGCGGTAACTCTCTGTCTCTCTCATATATGCCACTTCTTTTAACCTCCCAAGAAATT | 1530 |
| Qy | | 1501 | TTTTTAAAATAAATATTTATAAT | 1522 |
| Db | | 1531 | TTTTTAAAATAAATATTTATAAT | 1552 |

RESULT 10
US-10-301-822-11
; Sequence 11, Application US/10301822
; Publication No. US20030148410A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MP001-029P2RNM
; CURRENT APPLICATION NUMBER: US/10/301,822
; CURRENT FILING DATE: 2002-11-21
; PRIORITY APPLICATION NUMBER: US 60/339,971
; PRIORITY FILING DATE: 2001-12-10
; PRIORITY APPLICATION NUMBER: US 60/361,978
; PRIORITY FILING DATE: 2002-03-05
; PRIORITY APPLICATION NUMBER: US 60/381,988
; PRIORITY FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 1552
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (43)...(1422)
US-10-301-822-11

| Query Match | 100.0.0%; | Score 1522; | DB 15; | Length 1552; |
|-----------------------|-----------------|--|-----------|--------------|
| Best Local Similarity | 100.0.0%; | Prod. No. 0; | | |
| Matches 1522; | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0; |
| QY | 1 | ACAGTCAGCGCATGGCTCCCGCTGGTCCCGCCAGAGCCCTGGCTCCCTCTGTTGATCCCGGCC | 60 | |
| DB | 31 | ACAGTCAGCGCATGGCTCCCGCTGGTCCCGCCAGAGCCCTGGCTCCCTCTGTTGATCCCGGCC | 90 | |
| QY | 61 | CTTGCTCCAGCGCTCACTGTGCACACTGCTGCTGTCACTGCTGCTTCTGTATGTCCTGTCAT | 120 | |
| DB | 91 | CTTGCTCCAGCGCTCACTGTGCACACTGCTGCTGTCACTGCTGCTTCTGTATGTCCTGTCAT | 150 | |
| QY | 121 | CCCAGAGGTTGCCCGGATGCAAGGAGATTCCCTCTGGGAGAGGCTCTTCTGGGGAA | 180 | |
| DB | 151 | CCCAGAGGTTGCCCGGATGCAAGGAGATTCCCTCTGGGAGAGGCTCTTCTGGGGAA | 210 | |
| QY | 181 | GATGACCCACTGGCGAGGAGGATCTGCCCAGTGAAGAGGATTCACCCAGAGAGGAGGAT | 240 | |
| DB | 211 | GATGACCCACTGGCGAGGAGGATCTGCCCAGTGAAGAGGATTCACCCAGAGAGGAGGAT | 270 | |
| QY | 241 | CCACCCGAGGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT | 300 | |
| DB | 271 | CCACCCGAGGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT | 330 | |
| QY | 301 | GAAGTTAAGCCTAAATCAGAAGAAGAGGGCTCCCTGAAATTAGAGGATCTACCTACTGTT | 360 | |
| DB | 331 | GAAGTTAAGCCTAAATCAGAAGAAGAGGGCTCCCTGAAATTAGAGGATCTACCTACTGTT | 390 | |
| QY | 361 | GAGCTCTCTGAGATCTCTCAAGAACCCAGAAATAATGCCACAGGGGCAAGAGGGGAT | 420 | |
| DB | 391 | GAGCTCTCTGAGATCTCTCAAGAACCCAGAAATAATGCCACAGGGGCAAGAGGGGAT | 450 | |
| QY | 421 | GACCAGAGTCAATTGGCGCTATGAGGGCGACCCGCGCTTGGCCCGGGGTGTCCTCCAGAGCTGC | 480 | |
| DB | 451 | GACCAGAGTCAATTGGCGCTATGAGGGCGACCCGCGCTTGGCCCGGGGTGTCCTCCAGAGCTGC | 510 | |
| QY | 481 | GCGGGCGCTTCCAGTCCCGCGTGGATATCCGCCCCCAGCTCGCGCGCTTCTGCGCGGCC | 540 | |

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Db 511 GCGGCGCGCTTCCAGTCCCGGTGGATATCGCCCCCAGCTCGCGCTTCTGCGCGGCC 570
Qy 541 CTGCGCGCGCTTGGAACTCTCTGGGCTTCAGAGTCCGCGCGCTCCAGAACTGCGCTCGC 600
Db 571 CTGCGCGCGCTTGGAACTCTCTGGGCTTCAGAGTCCGCGCGCTCCAGAACTGCGCTCGC 630
Qy 601 AACAAATGGCCACAGTGTGCAACTGACCTGCTCTCTGGGCTAGAGATGGCTCTGGGTCCC 660
Db 631 AACAAATGGCCACAGTGTGCAACTGACCTGCTCTCTGGGCTAGAGATGGCTCTGGGTCCC 690
Qy 661 GGGCGGAGTACCGGGCTCTGACAGTGCATCTGCACTGGGGGGTGCAGGTGCTCGCGGC 720
Db 691 GGGCGGAGTACCGGGCTCTGACAGTGCATCTGCACTGGGGGGTGCAGGTGCTCGCGGC 750
Qy 721 TCGGAGCACACTGTGGAGGCCACGCTTCCCTGCGGAGATCCAGGTGCTCACTCAGC 780
Db 751 TCGGAGCACACTGTGGAGGCCACGCTTCCCTGCGGAGATCCAGGTGCTCACTCAGC 810
Qy 781 ACCGCTTTGCGACAGTTGACAGGCCCTTGGGGGCGCGGAGGCTTGGCGTGTGGCC 840
Db 811 ACCGCTTTGCGACAGTTGACAGGCCCTTGGGGGCGCGGAGGCTTGGCGTGTGGCC 870
Qy 841 GCCTTTCTGGAGGAGGCCCGGAAAGAAACAGTGCCTATGAGCAGTTGCTGTCTGCGTTG 900
Db 871 GCCTTTCTGGAGGAGGCCCGGAAAGAAACAGTGCCTATGAGCAGTTGCTGTCTGCGTTG 930
Qy 901 GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGAGTCCAGGATCCAGGATATCTGCACTC 960
Db 931 GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCTCCAGGACTGGAACATCTGCACTC 990
Qy 961 CTGCGCTCTGACTTCAAGCGCTACTTCCAATATGAGGGGTCTCTGACTACACGCGCCGTG 1020
Db 991 CTGCGCTCTGACTTCAAGCGCTACTTCCAATATGAGGGGTCTCTGACTACACGCGCCGTG 1050
Qy 1021 GCCAGGGTGTCACTTGGAAGTGTGTTTAAACAGACAGTGTGCTGAGTGTCTAAAGCAGCTC 1080
Db 1051 GCCAGGGTGTCACTTGGAAGTGTGTTTAAACAGACAGTGTGCTGAGTGTCTAAAGCAGCTC 1110
Qy 1081 CACACCTCTCTGACACCTCTGCGGACCTGCTGACTCTCGGCTACAGCTGAATCCGA 1140
Db 1111 CACACCTCTCTGACACCTCTGCGGACCTGCTGACTCTCGGCTACAGCTGAATCCGA 1170
Qy 1141 GCAGCAGCAGCTTTGAATGGCGAGTGAATGAGGCTCTTCCCTGCTGGAGTGGACAGC 1200
Db 1171 GCAGCAGCAGCTTTGAATGGCGAGTGAATGAGGCTCTTCCCTGCTGGAGTGGACAGC 1230
Qy 1201 AGTCTCGGGCTGCTGAGCAGTCCAGTGAATTCCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
Db 1231 AGTCTCGGGCTGCTGAGCAGTCCAGTGAATTCCTGCTGCTGCTGCTGCTGCTGCTGCT 1290
Qy 1261 GCGCTGCTTTTGGCTCTCTTTGCTGCTCAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
Db 1291 GCGCTGCTTTTGGCTCTCTTTTGTCTGCTCAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCT 1350
Qy 1321 AGGAGCAGCAGAGAGGGAACCAAGAGGGGTGTGAGTACCGCCAGCAGAGGTAGCCGAG 1380
Db 1351 AGGAGCAGCAGAGAGGGAACCAAGAGGGGTGTGAGTACCGCCAGCAGAGGTAGCCGAG 1410
Qy 1381 ACTGAGCCTAGAGGCTGAGTCTTTGGAGAAATGTGAGAAAGCCAGCAGAGGCTCTGAGGG 1440
Db 1411 ACTGAGCCTAGAGGCTGAGTCTTTGGAGAAATGTGAGAAAGCCAGCAGAGGCTCTGAGGG 1470
Qy 1441 GGAGCGGGTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
Db 1471 GGAGCGGGTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1530
Qy 1501 TTTTAAATATAATTTATAT 1522
Db 1531 TTTTAAATATAATTTATAT 1552
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US-10-465-572-9
; Sequence 9, Application US/10465572
; Publication No. US20030207840A1
; GENERAL INFORMATION:
; APPLICANT: Riggs, Gregory
; APPLICANT: Lal, Anita
; TITLE OF INVENTION: GENES INDUCED BY HYPOXIA
; FILE REFERENCE: 000250.00012
; CURRENT APPLICATION NUMBER: US/10/465,572
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US/10/201,642
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: 60/307,600
; PRIOR FILING DATE: 2001-07-26
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1552
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-465-572-9
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Query Match 100.0%; Score 1522; DB 16; Length 1552;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 ACAGTCAGCGCATGGCTCCCTGTGCGCCAGCGCCCTGCTCTGTTGATCCCGGCC 60
Db 31 ACAGTCAGCGCATGGCTCCCTGTGCGCCAGCGCCCTGCTCTGTTGATCCCGGCC 90
Qy 61 CTGCTCCAGCGCTCACTGTGCAACTGCTGCTCACTGCTCTTCTGATGCTCTCAT 120
Db 91 CTGCTCCAGCGCTCACTGTGCAACTGCTGCTCACTGCTCTTCTGATGCTCTCAT 150
Qy 121 CCCAGAGTGTGCCCCGATGCAAGGAGATTCCTCCCTTGGAGAGAGCTCTTCTGGGAA 180
Db 151 CCCAGAGTGTGCCCCGATGCAAGGAGATTCCTCCCTTGGAGAGAGCTCTTCTGGGAA 210
Qy 181 GATGACCACTGGCGGAGGAGGATCTGCCAGTGAAGAGATTCACCCAGAGAGAGAT 240
Db 211 GATGACCACTGGCGGAGGAGGATCTGCCAGTGAAGAGATTCACCCAGAGAGAGAT 270
Qy 241 CCACCGGAGAGAGGATCTACCTGGAGAGAGGATCTACCTGGAGAGAGGATCTACCT 300
Db 271 CCACCGGAGAGAGGATCTACCTGGAGAGAGGATCTACCTGGAGAGAGGATCTACCT 330
Qy 301 GAAGTTAAGCTTAAATCAGAAAGAGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT 360
Db 331 GAAGTTAAGCTTAAATCAGAAAGAGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT 390
Qy 361 GAGGCTCTGGAGATCTCAAGAACCCCAAGATTAATGCCACAGGGACAAGAGGGAT 420
Db 391 GAGGCTCTGGAGATCTCAAGAACCCCAAGATTAATGCCACAGGGACAAGAGGGAT 450
Qy 421 GACACAGATCAATTGGCGCTATGAGGCGACCCCGCTTGGCCCGGGGTGTCCCAAGCTGC 480
Db 451 GACACAGATCAATTGGCGCTATGAGGCGACCCCGCTTGGCCCGGGGTGTCCCAAGCTGC 510
Qy 481 GCGGGCGCTTTCAGTCCCGGTGGATATCCGCCCCCAGCTGCGCCCTTCTGCGCGGCC 540
Db 511 GCGGGCGCTTTCAGTCCCGGTGGATATCCGCCCCCAGCTGCGCCCTTCTGCGCGGCC 570
Qy 541 CTGCGCCCCCTGGAATCTCTGGGCTTCCAGCTCCGCGCGCTCCAGAACTGCGCTCGGC 600
Db 571 CTGCGCCCCCTGGAATCTCTGGGCTTCCAGCTCCGCGCGCTCCAGAACTGCGCTCGGC 630
Qy 601 AACAAATGGCCACAGTGTGCAACTGACCTGCTCTCTGGGCTAGAGATGGCTCTGGGTCCC 660
Db 631 AACAAATGGCCACAGTGTGCAACTGACCTGCTCTCTGGGCTAGAGATGGCTCTGGGTCCC 690
Qy 661 GGGCGGAGTACCGGGCTCTGCACTGCACTGCGAGTGCAGGTGCTCGCGGC 720
Db 691 GGGCGGAGTACCGGGCTCTGCACTGCACTGCGAGTGCAGGTGCTCGCGGC 750
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QY 721 TCGGAGCACACTGTGGAGGCGCACCGTTTCCCTGCGGAGATCCAGTGTGTTCACTCTCAGC 780
DB 751 TCGGAGCACACTGTGGAGGCGCACCGTTTCCCTGCGGAGATCCAGTGTGTTCACTCTCAGC 810
QY 781 ACCGCTTTTCCAGAGATTTGACAGAGGCTTTGGGCGCGCCGGAGGCTGTGCTGTGCGC 840
DB 811 ACCGCTTTTCCAGAGATTTGACAGAGGCTTTGGGCGCGCCGGAGGCTGTGCTGTGCGC 870
QY 841 GCTTTTCCAGAGGCGCGCGGAGGAGAAACAGTGTGCTATGAGCAGTGTGCTGTGCTGTG 900
DB 871 GCTTTTCCAGAGGCGCGCGGAGGAGAAACAGTGTGCTATGAGCAGTGTGCTGTGCTGTG 930
QY 901 GAAGAAATCGCTGAGAGGCTCAGAGACTCAGAGTCCAGGACTGACATATCTGCACTC 960
DB 931 GAAGAAATCGCTGAGAGGCTCAGAGACTCAGGTTCCAGGACTGACATATCTGCACTC 990
QY 961 CTGCTCTCTGACTTTCAGCGGCTACTTCCAAATATGAGGGTCTCTGACTACACCGCCTGT 1020
DB 991 CTGCTCTCTGACTTTCAGCGGCTACTTCCAAATATGAGGGTCTCTGACTACACCGCCTGT 1050
QY 1021 GCCCAGGCTGCTATCTGAGTGTGTTTAAACAGAGATGCTGAGTGTCTTAAGCAGCTC 1080
DB 1051 GCCCAGGCTGCTATCTGAGTGTGTTTAAACAGAGATGCTGAGTGTCTTAAGCAGCTC 1110
QY 1081 CACACCTCTCTGACACCTGTGGGACCTGTGACTCTCGGCTACAGTGAACCTCCGA 1140
DB 1111 CACACCTCTCTGACACCTGTGGGACCTGTGACTCTCGGCTACAGTGAACCTCCGA 1170
QY 1141 GCGAGCAGCCTTTGAATGGGCGAGTATTGAGGCTCTCTCCCTGCTGAGTGGACAGC 1200
DB 1171 GCGAGCAGCCTTTGAATGGGCGAGTATTGAGGCTCTCTCCCTGCTGAGTGGACAGC 1230
QY 1201 AGTCTCTGCGGCTGCTGAGCAGTCCAGCTCAGCTGAATTTCTGCTGCTGCTGCTGCTA 1260
DB 1231 AGTCTCTGCGGCTGCTGAGCAGTCCAGCTGAATTTCTGCTGCTGCTGCTGCTA 1290
QY 1261 GCTCTGCTTTTGGCTCTCTTTTGTGTCACAGGCTGCTGCTGCTGCTGCTGCTGCTG 1320
DB 1291 GCTCTGCTTTTGGCTCTCTTTTGTGTCACAGGCTGCTGCTGCTGCTGCTGCTGCTG 1350
QY 1321 AGCAGCAGCAGAGGAGGAAACCAAGGGGTGTGAGTACCGCCAGCAGAGGTAGCCGAG 1380
DB 1351 AGCAGCAGCAGAGGAGGAAACCAAGGGGTGTGAGTACCGCCAGCAGAGGTAGCCGAG 1410
QY 1381 ACTGAGCCTAGAGGCTGATCTTTGAGAAATGTGAGAAACCAAGGCACTCTGAGGG 1440
DB 1411 ACTGAGCCTAGAGGCTGATCTTTGAGAAATGTGAGAAACCAAGGCACTCTGAGGG 1470
QY 1441 GGAGCGGTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
DB 1471 GGAGCGGTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1530
QY 1501 TTTTAAATAAATAATTTATAAT 1522
DB 1531 TTTTAAATAAATAATTTATAAT 1552

RESULT 12
US-10-295-027-305
; Sequence 305, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Nataasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.

; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 305
; LENGTH: 1552
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-295-027-305

Query Match 100.0%; Score 1522; DB 16; Length 1552;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAGTCACGCGCAGTGGCTCCCTGTCGCCAGCCCTGGCTCCCTCTGTGTATCCCGCC 60
DB 31 ACAGTCACGCGCAGTGGCTCCCTGTCGCCAGCCCTGGCTCCCTCTGTGTATCCCGCC 90
QY 61 CTGTCTCAGGCTCACTGTGCACTGTGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGT 120
DB 91 CTGTCTCAGGCTCACTGTGCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 150
QY 121 CCCAGAGGTTGCCCCGATGAGAGGATTTCCCTTTGGAGAGGCTCTTTCTGGGAA 180
DB 151 CCCAGAGGTTGCCCCGATGAGAGGATTTCCCTTTGGAGAGGCTCTTTCTGGGAA 210
QY 181 GATGACCCACTGGGCGAGGAGGATCTGCCAGTGAAGAGGATTCACCCAGAGAGGAGAT 240
DB 211 GATGACCCACTGGGCGAGGAGGATCTGCCAGTGAAGAGGATTCACCCAGAGAGGAGAT 270
QY 241 CCACCCGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT 300
DB 271 CCACCCGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT 330
QY 301 GAAGTTAAGCCCTAAATCAGAAAGAGAGGCTCCCTGTGAAGTTAGAGATCTACTACTGTT 360
DB 331 GAAGTTAAGCCCTAAATCAGAAAGAGAGGCTCCCTGTGAAGTTAGAGATCTACTACTGTT 390
QY 361 GAGGCTCTGGAGATCTCTCAGAACCCAGATATATGCCAGAGGAGGAGGAGGAT 420
DB 391 GAGGCTCTGGAGATCTCTCAGAACCCAGATATATGCCAGAGGAGGAGGAGGAT 450
QY 421 GACACAGAGTCAATTGGCGCTATGGAGGCGACCCCGCTGCGCCCGGCTGTCCCGAGCTGC 480
DB 451 GACACAGAGTCAATTGGCGCTATGGAGGCGACCCCGCTGCGCCCGGCTGTCCCGAGCTGC 510
QY 481 GCGGCGCGCTTCCAGTCCCGCTGATATTCGCGCCCGCTGCTGCGCGCTTCTGCGCGGCC 540
DB 511 GCGGCGCGCTTCCAGTCCCGCTGATATTCGCGCCCGCTGCTGCGCGCTTCTGCGCGGCC 570

Db 541 CGCCCTGGAACTCTCTGGGCTTCAGCTCCGCGCTCCAGAACTGGGCTGGCAAC 600
Qy 604 AATGCCACAGTGTGCAACTGACCTGCTCTCTGGGCTAGAGATGGCTCTGGGTCCTGGG 663
Db 601 AATGCCACAGTGTGCAACTGACCTGCTCTCTGGGCTAGAGATGGCTCTGGGTCCTGGG 660
Qy 664 CGGAGTACCGGGCTCTGACGCTGATCTGACCTGAGGGGCTGAGGTCGTCGGGGCTCG 723
Db 661 CGGAGTACCGGGCTCTGACGCTGATCTGACCTGAGGGGCTGAGGTCGTCGGGGCTCG 720
Qy 724 GAGCACACTGTGGAGGCACTGCTTCCCTGCGAGATCCACGTGGTTTCACTCAGCAAC 783
Db 721 GAGCACACTGTGGAGGCACTGCTTCCCTGCGAGATCCACGTGGTTTCACTCAGCAAC 780
Qy 784 GCCTTTGCGAGTTGACAGGCTTGGGGCTGGGGCGCCCGGAGGCTGGGCTGTTGGCGGCC 843
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Db 1141 ACGCAGCCTTTGAAATGGGCGAGTGAATGAGGCTCTCTTCCCTGCTGGAGTGGACAGCAGT 1200
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RESULT 15
US-09-783-708-2
; Sequence 2, Application US/09783708
; Patent No. US20020058041A1
; GENERAL INFORMATION:

; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: KIDNEY-SPECIFIC TUMOR VACCINE DIRECTED AGAINST KIDNEY TUMOR ANTIGEN
; FILE REFERENCE: 366T-897420US
; CURRENT APPLICATION NUMBER: US/09/783,708
; CURRENT FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 60/182,429
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 60/182,636
; PRIOR FILING DATE: 2000-02-15
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 1833
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Nucleic acid encoding G250-GM-CSF fusion protein with His tag
US-09-783-708-2

Query Match 90.7%; Score 1379.8; DB 9; Length 1833;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1381; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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